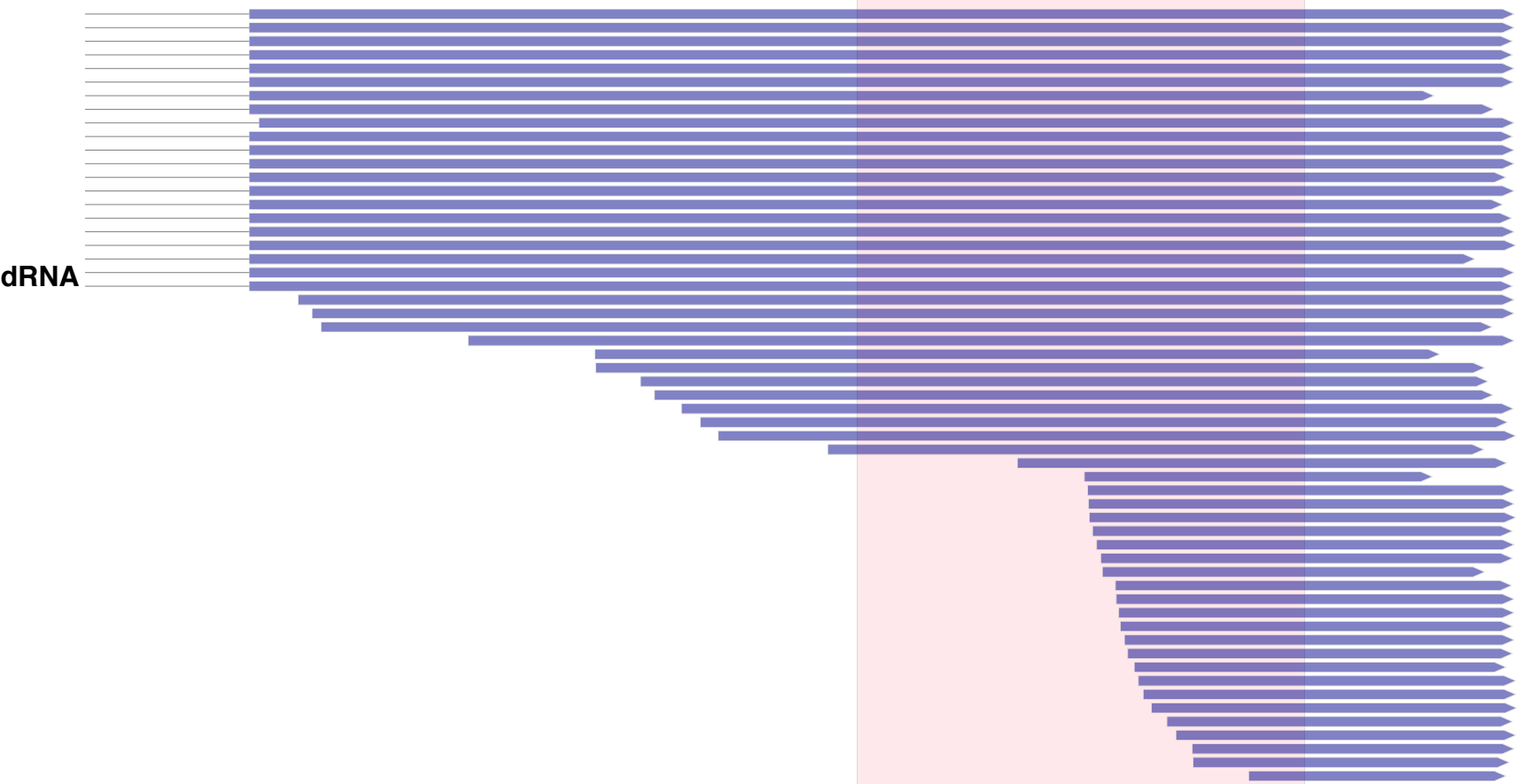
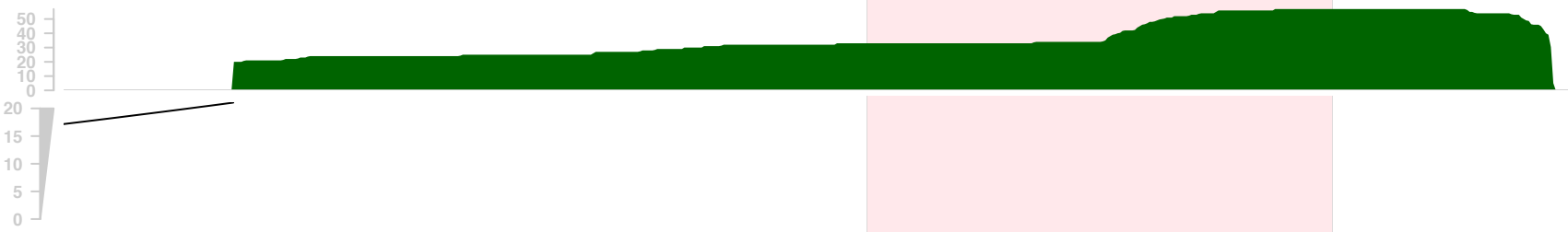
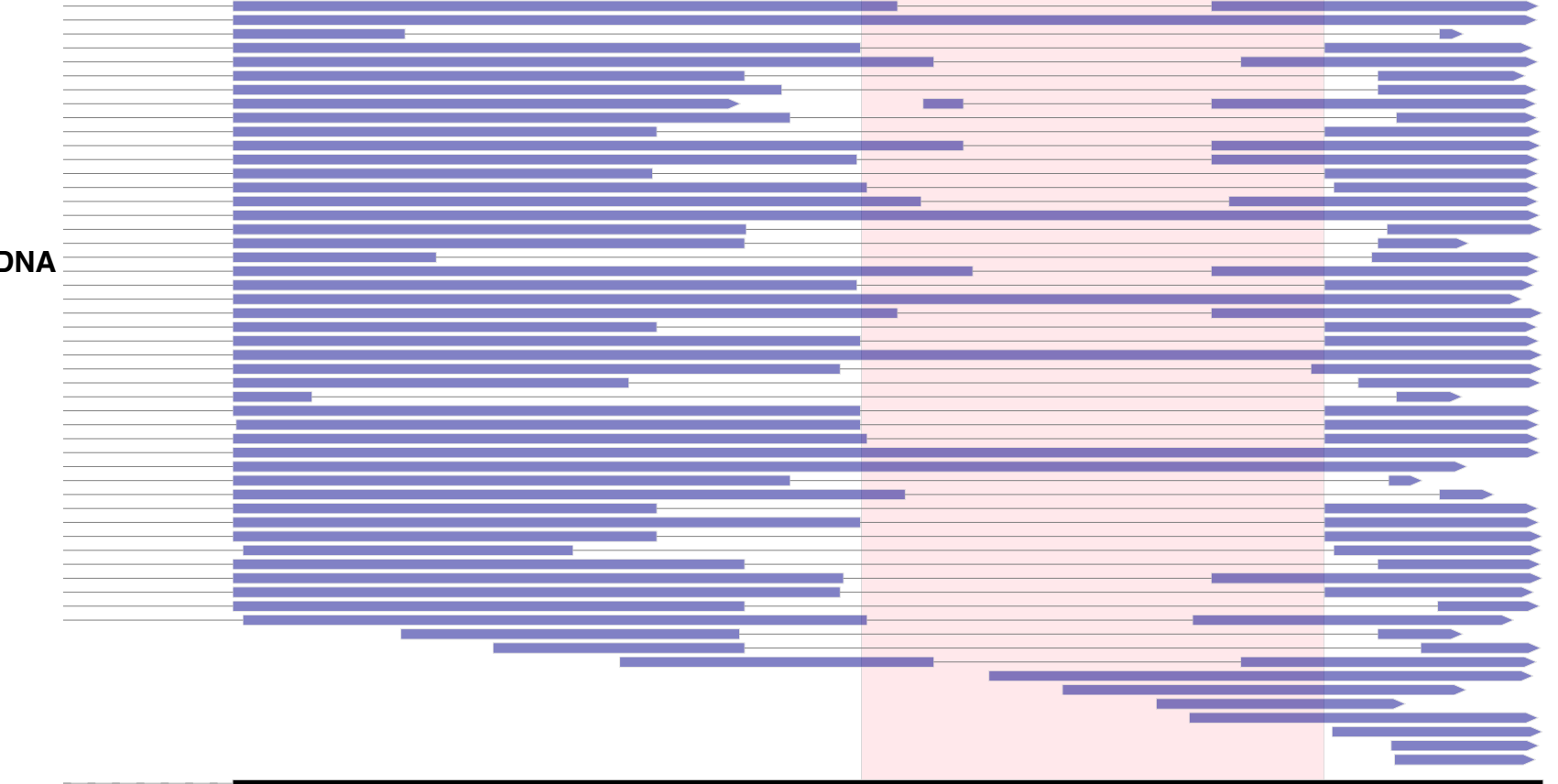
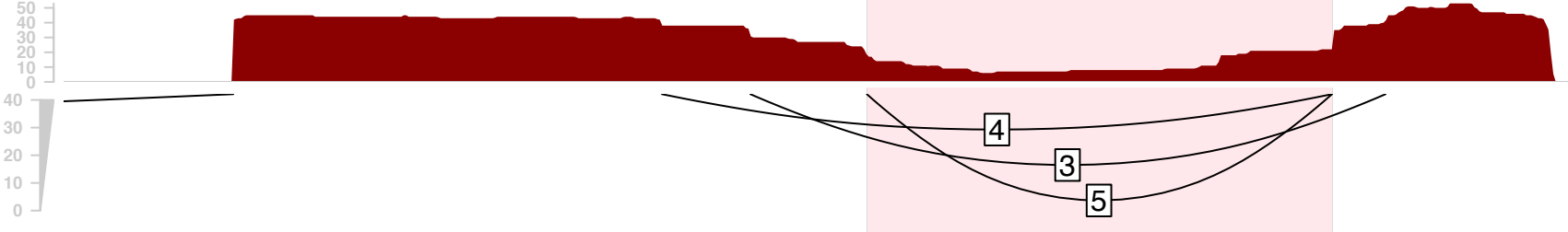
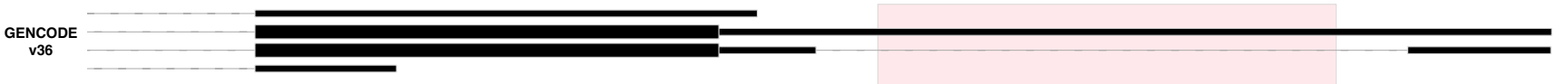


Data 1. Putative falsitrons in the genomic context. Genome browser view for 100 falsitron events that were detected in long-read ONT sequencing data produced by the Nanopore RNA Consortium and the Singapore Nanopore Expression Project (SG-NEx). For each event, the title provides the genomic coordinates (human genome version hg38), the gene symbol, the cell line in which the event was detected, and the direct repeat sequence if any. Each plot includes the following tracks: (i) reference transcript models (GENCODE v36), (ii) cDNA-seq read coverage (red), (iii) cDNA-seq sashimi plot of splice junctions, (iv) cDNA-seq transcript annotation (StringTie), (v) dRNA-seq read coverage (green), (vi) dRNA-seq sashimi plot of splice junctions, (vii) dRNA-seq transcript annotation (StringTie). The same tracks are also provided for dcDNA-seq (orange) if available. The position of the putative falsitron is highlighted in light red. For the sashimi plots, only junctions supported by a minimum of five reads are shown. Note that 11 events were detected in the comparison of both cDNA-seq and dcRNA-seq against dRNA-seq and are hence depicted on the same page.

chr1:28335161-28335708:+ MED18

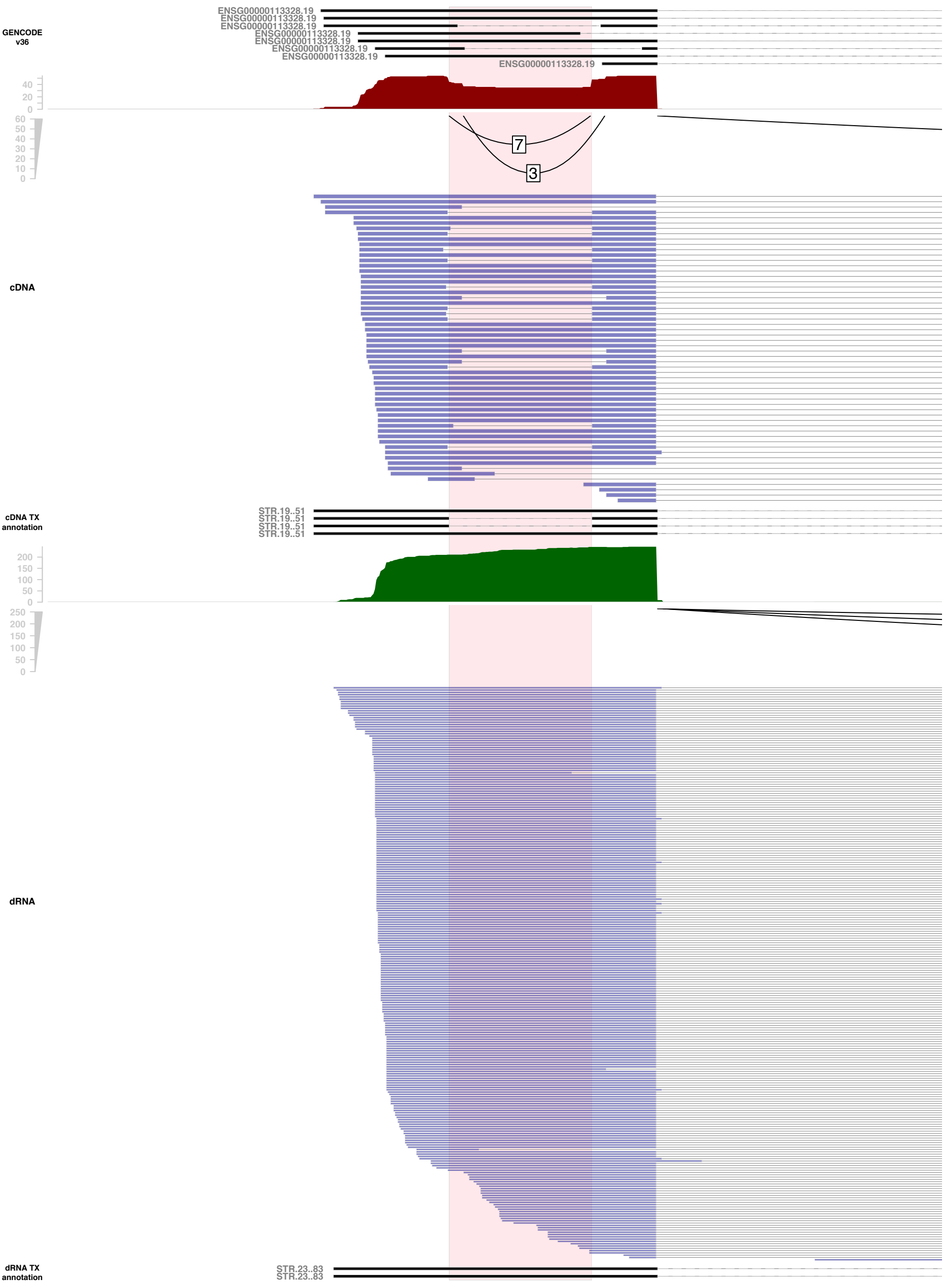
Cell line: A549

Direct repeat sequence: CAGC



chr5:163437659-163437758:+ CCNG1

Cell line: A549



chr8:47976979-47977736:+ MCM4

Cell line: A549

GENCODE
v36

ENSG00000104738.18

100
50
0
70
60
50
40
30
20
10
0

6

cDNA

cDNA TX
annotation

600
400
200
0
600
500
400
300
200
100
0

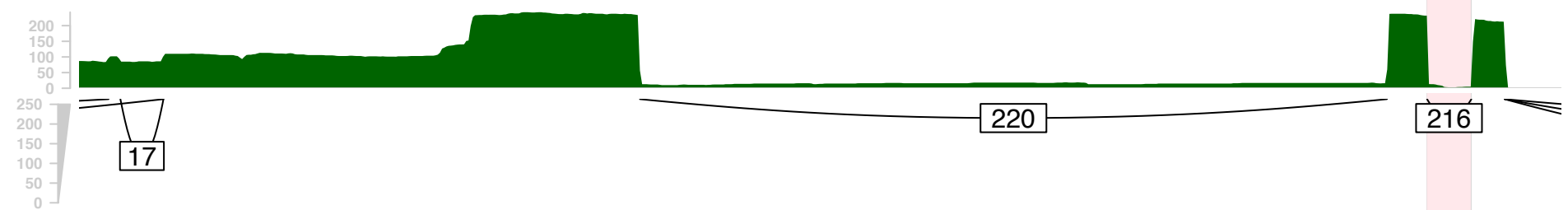
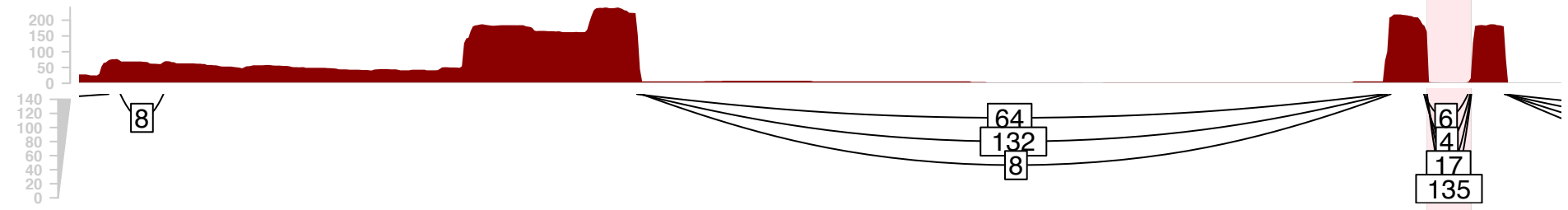
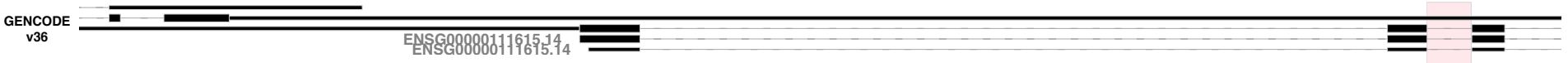
dRNA

dRNA TX
annotation



chr12:75501816-75501921:+ GLIPR1

Cell line: A549

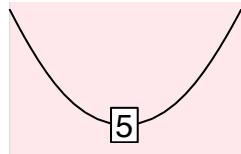


chr15:63121977-63122084:+ LACTB

Cell line: A549

GENCODE
v36

ENSG00000103642.12
ENSG00000103642.12



2

cDNA



cDNA TX
annotation

STR.48..200
STR.48..200
STR.48..200



2

dRNA



dRNA TX
annotation

STR.62..201
STR.62..201
STR.62..201

chr17:3663563-3663657:- TAX1BP3,P2RX5-TAX1BP3

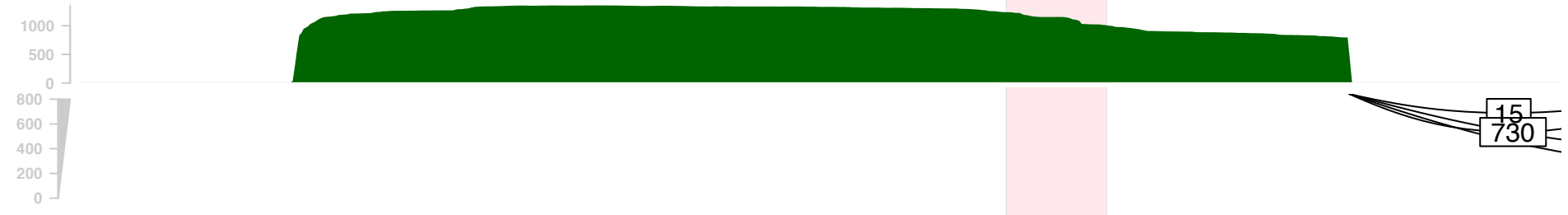
Cell line: A549

Direct repeat sequence: GACCG

GENCODE v36
ENSG00000213977.8
ENSG00000213977.8
ENSG00000257950.3



cDNA TX annotation
STR.53..115

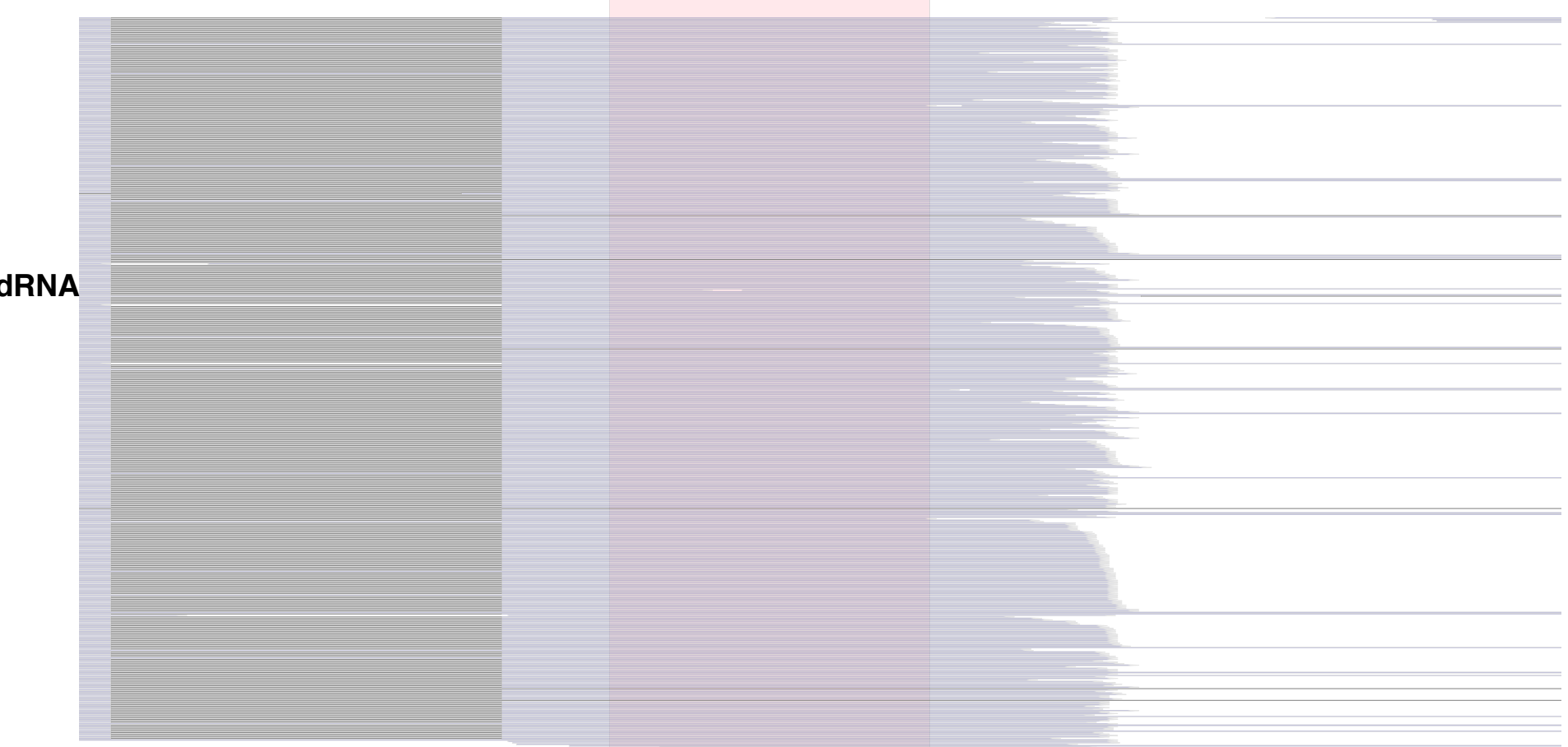
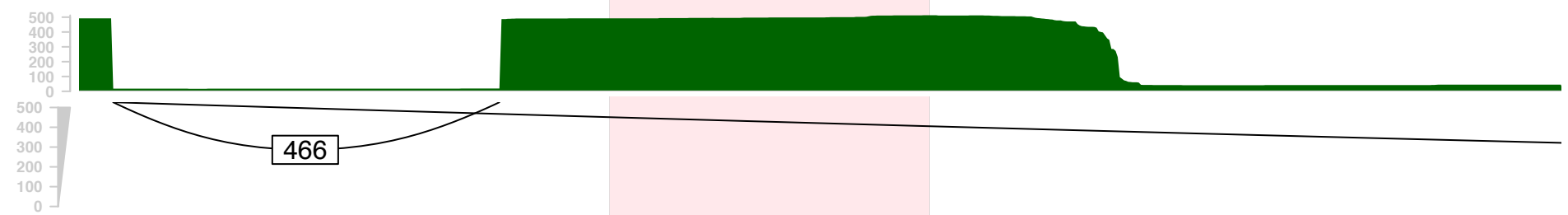
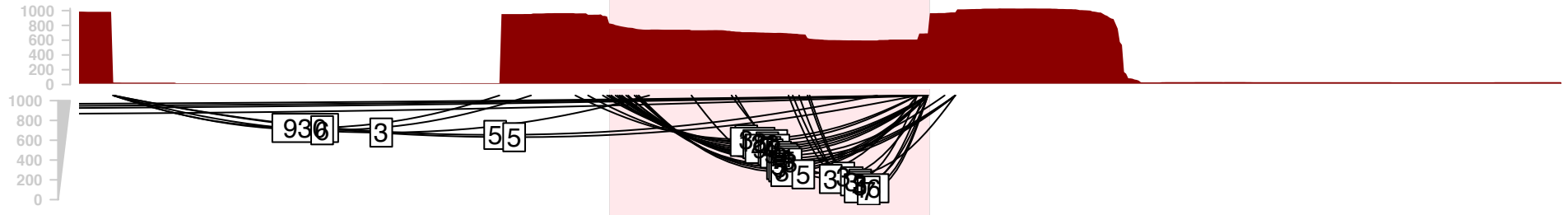


dRNA TX annotation
STR.69..62

chr19:35746759-35746910:+ PSENN,AC002398.9

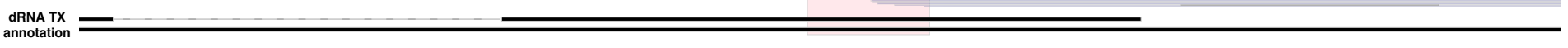
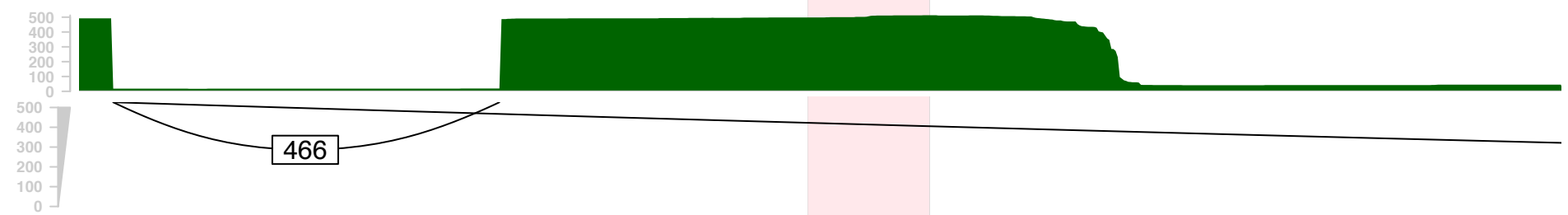
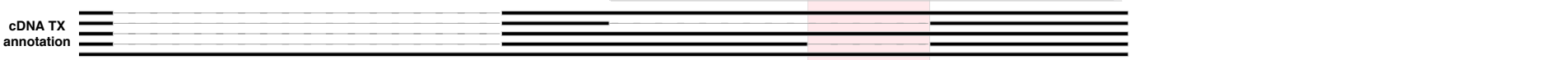
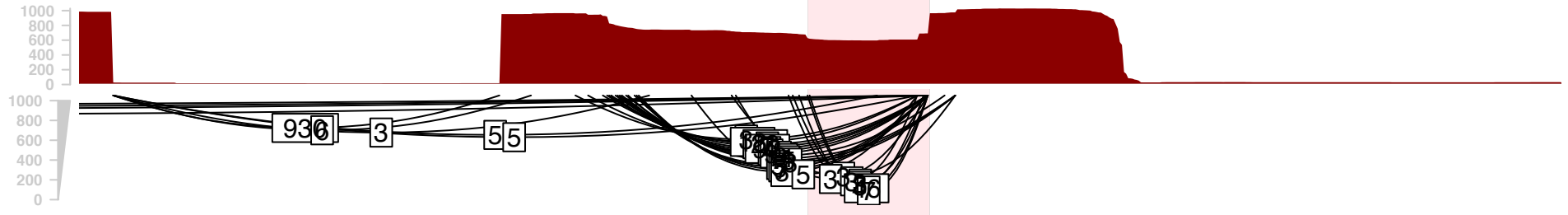
Cell line: A549

Direct repeat sequence: CCTG



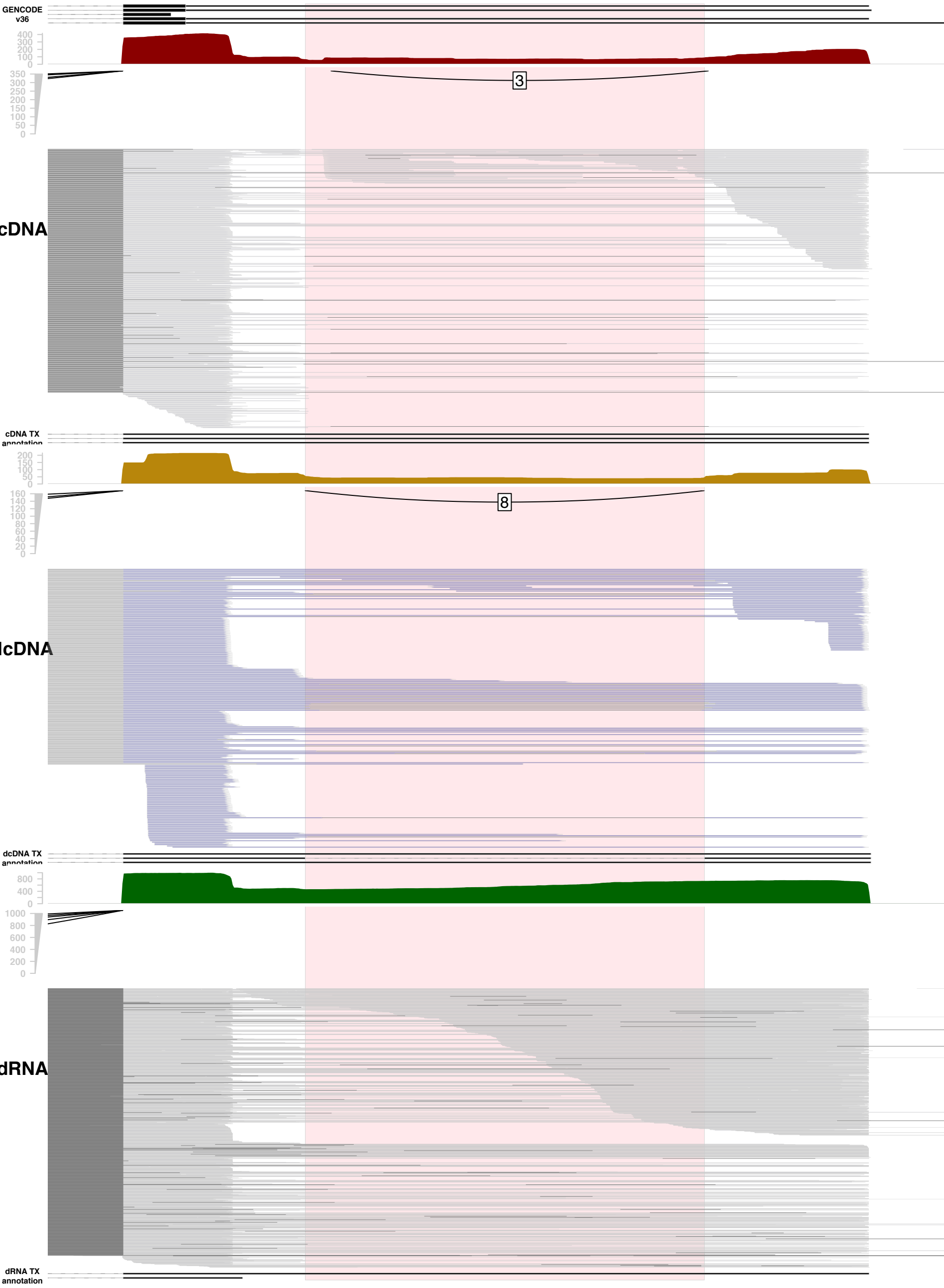
chr19:35746853-35746910:+ PSENN,AC002398.9

Cell line: A549



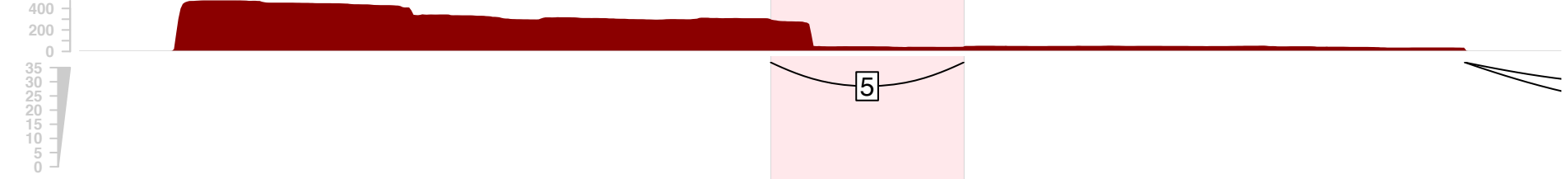
chr4:56459858-56460922:+ PAICS

Cell line: A549



chr1:8012958-8013358:- ERRFI1
Cell line: Hct116
Direct repeat sequence: GGGAAGC

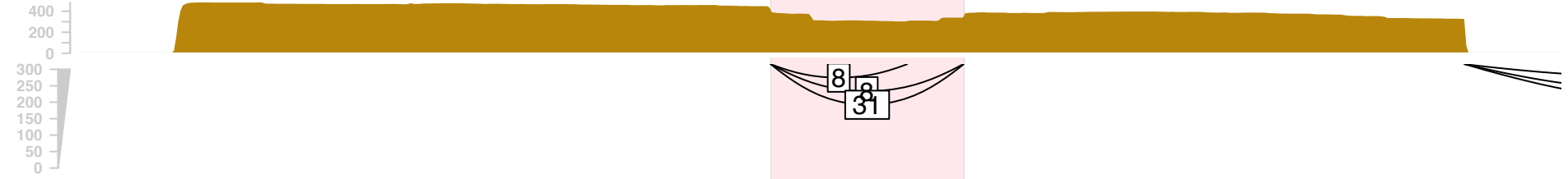
GENCODE 0116285.13 v36
ENSG00000116285.12
ENSG00000116285.13
ENSG00000116285.13



cDNA



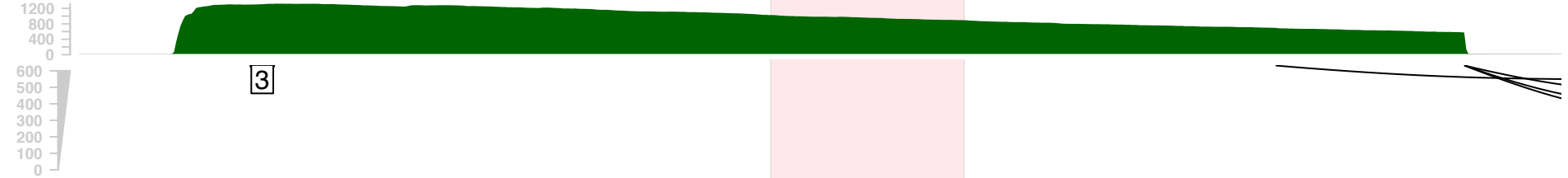
cDNA TX annotation 1:136
1:138



cDNA



dcDNA TX annotation 1:136
1:138



dRNA

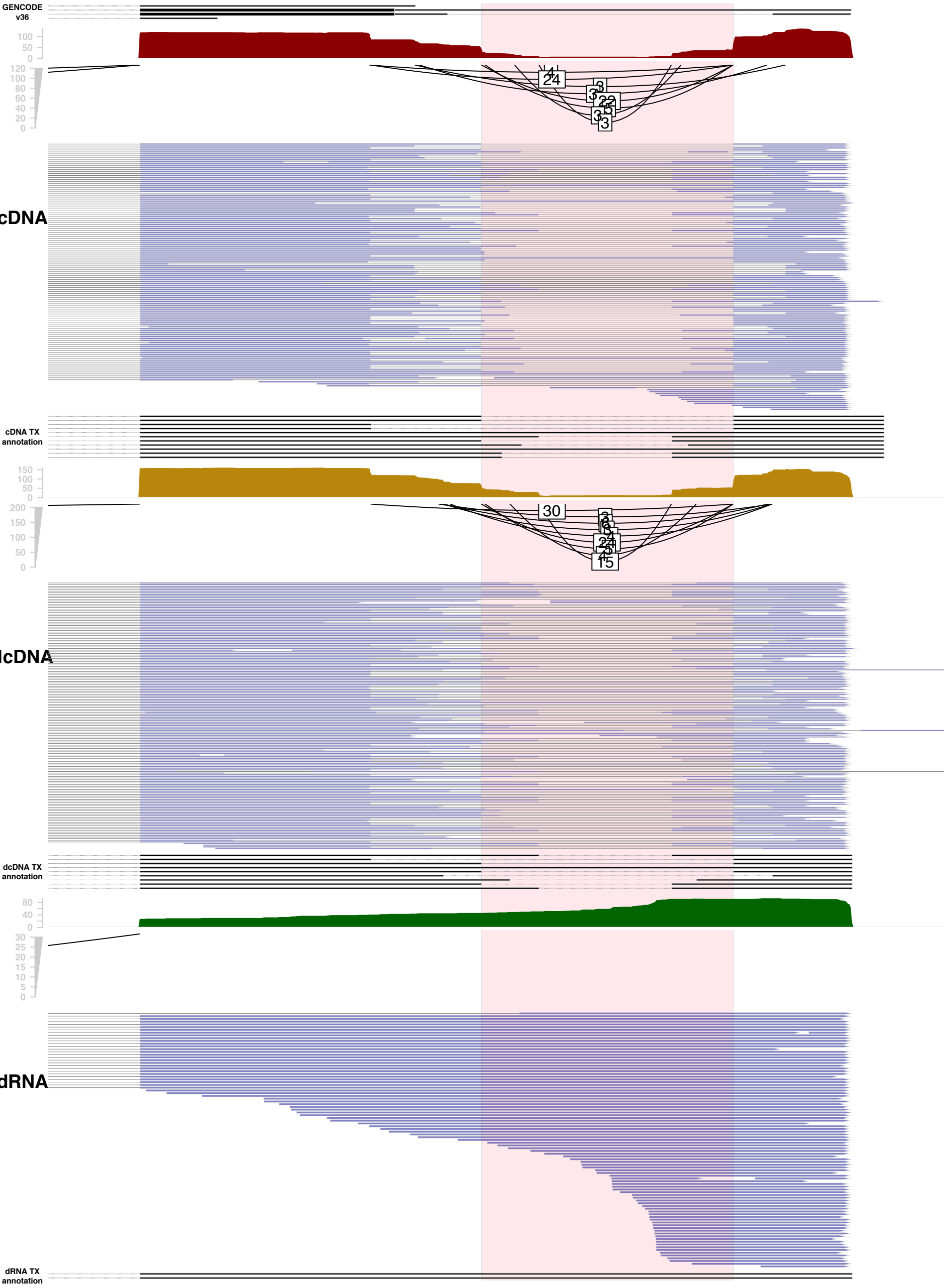


dRNA TX annotation 1:136
1:138

chr1:28335161-28335708:+ MED18

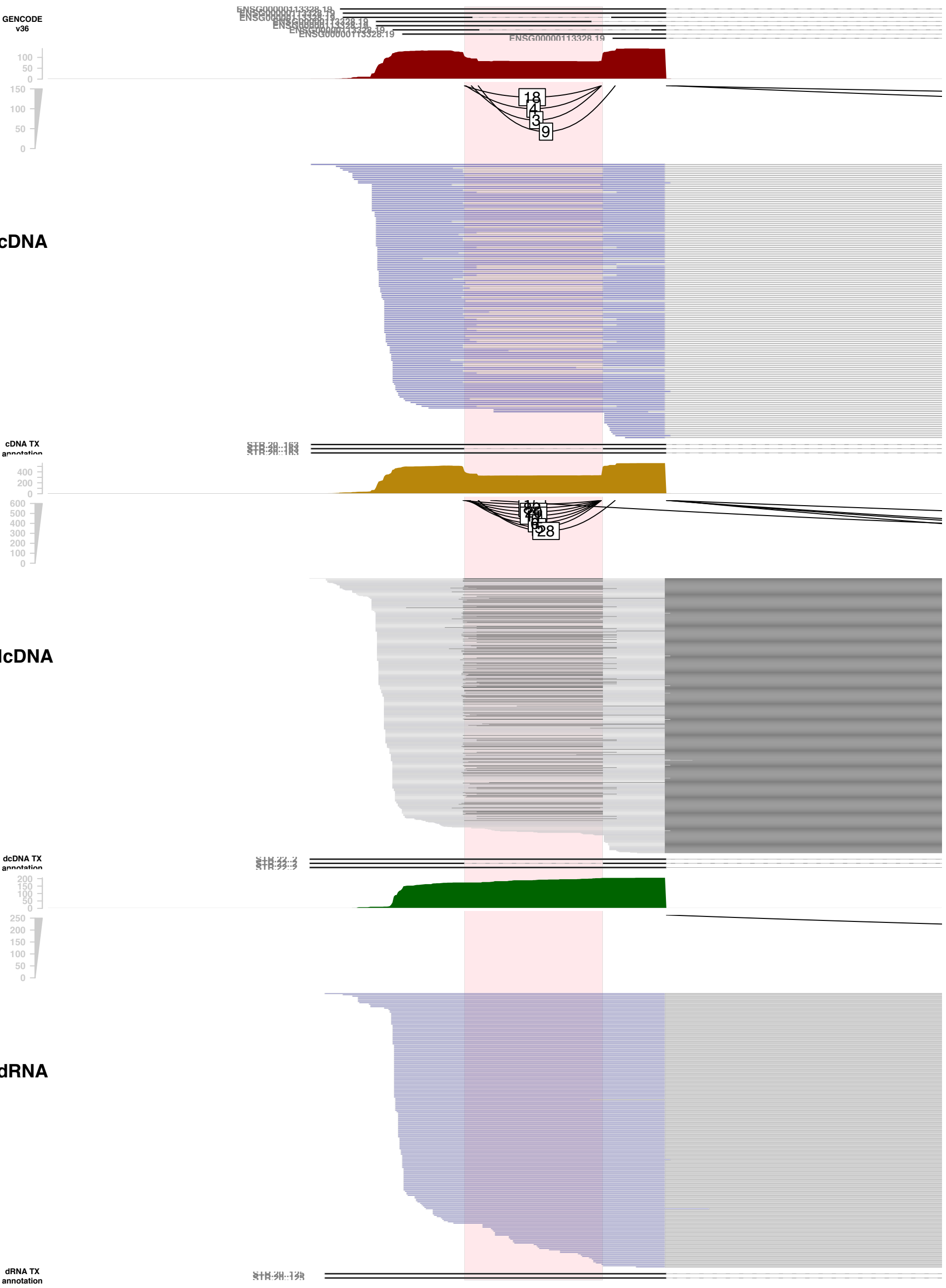
Cell line: Hct116

Direct repeat sequence: CAGC



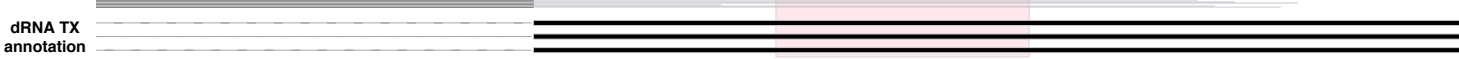
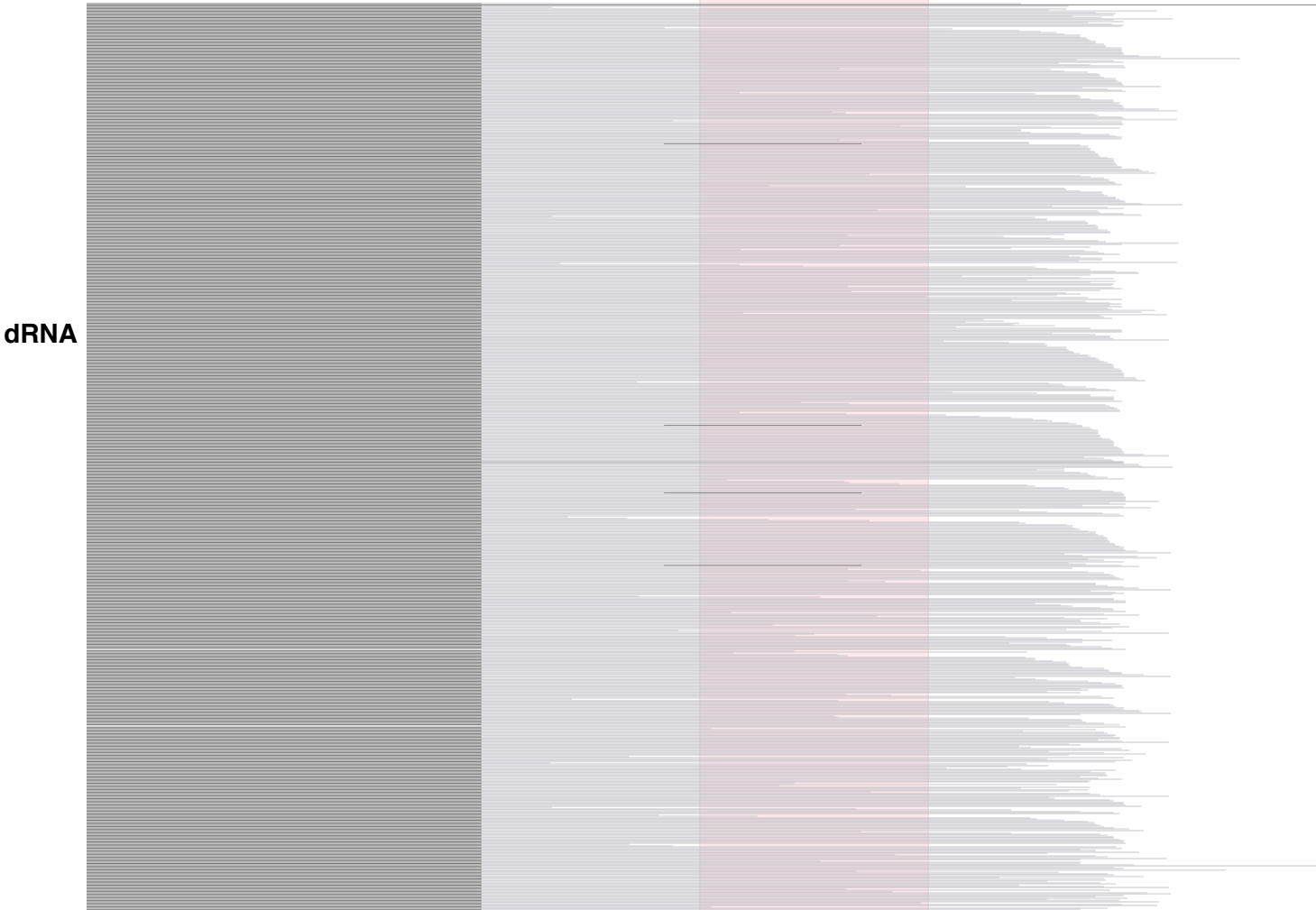
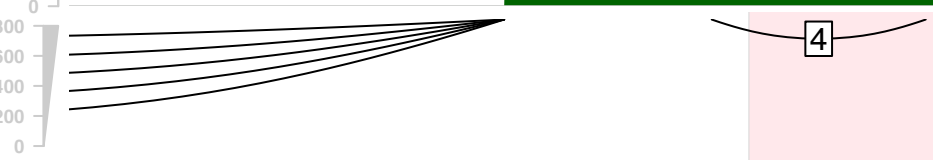
chr5:163437659-163437758:+ CCNG1

Cell line: Hct116



chr6:170584410-170584525:- PDCD2

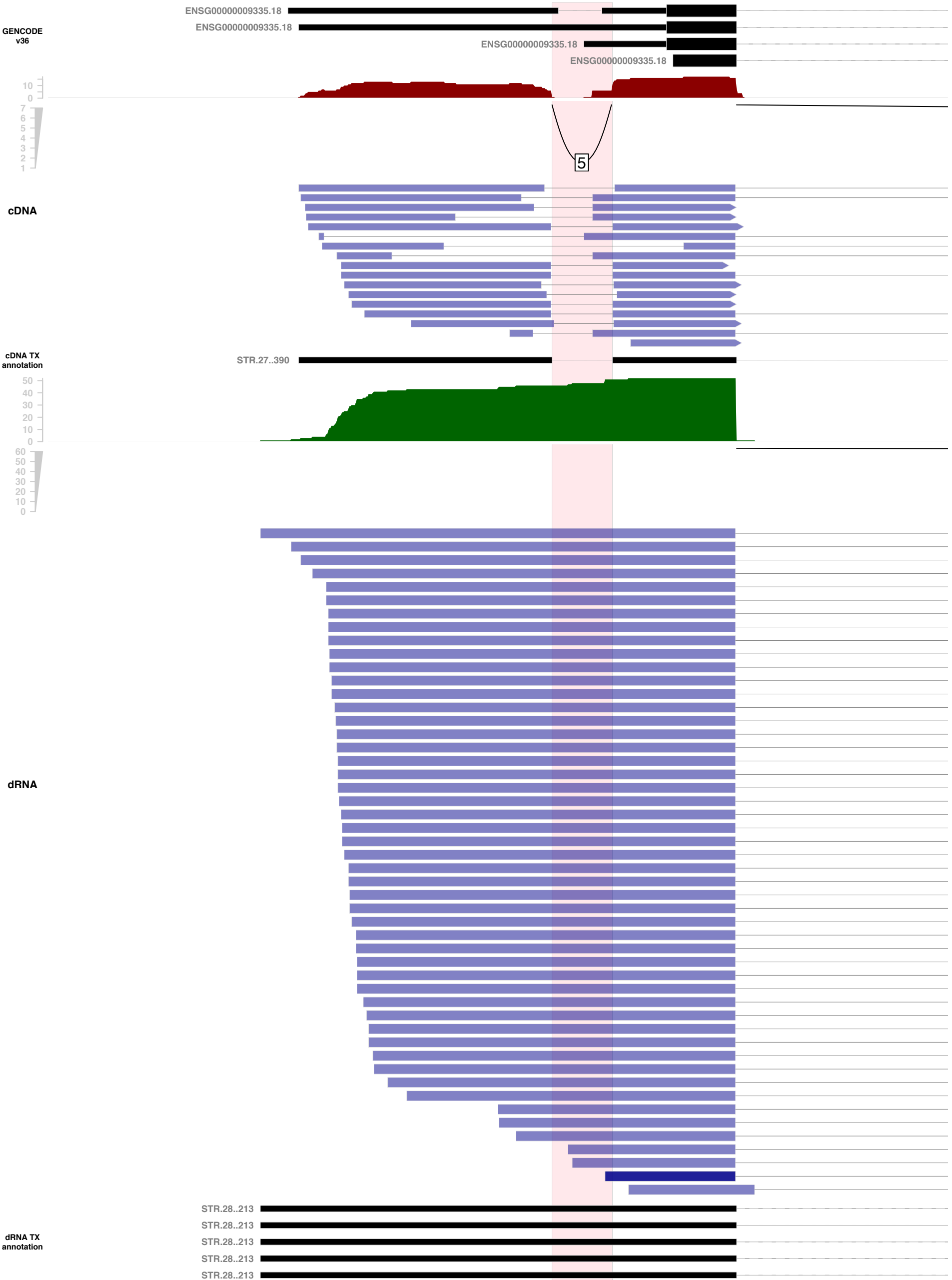
Cell line: Hct116



chr7:157139165-157139221:+ UBE3C

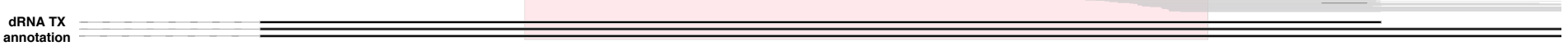
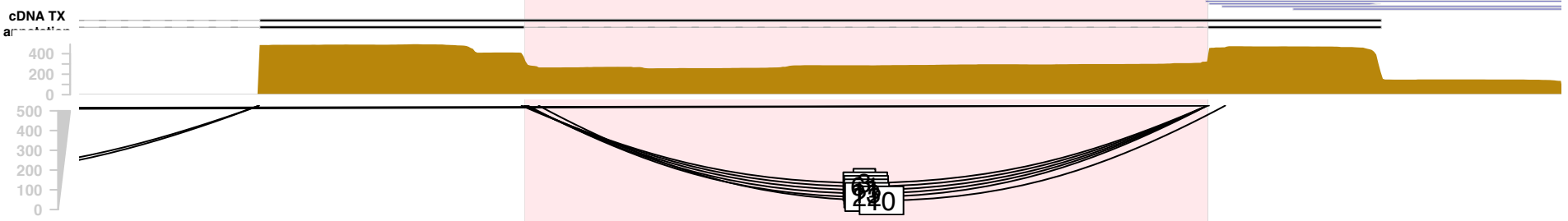
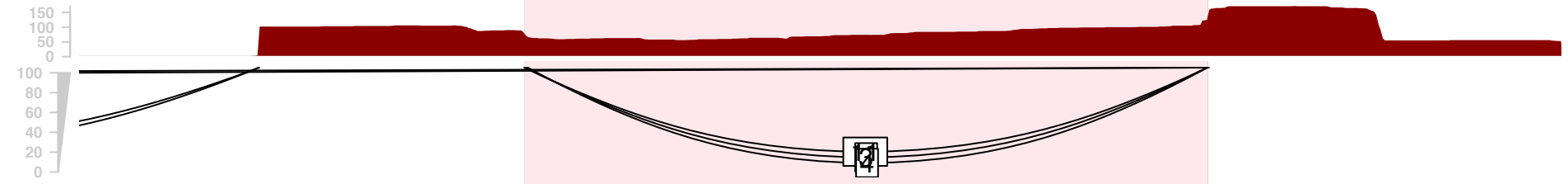
Cell line: Hct116

Direct repeat sequence: GCCC



chr8:47976979-47977736:+ MCM4

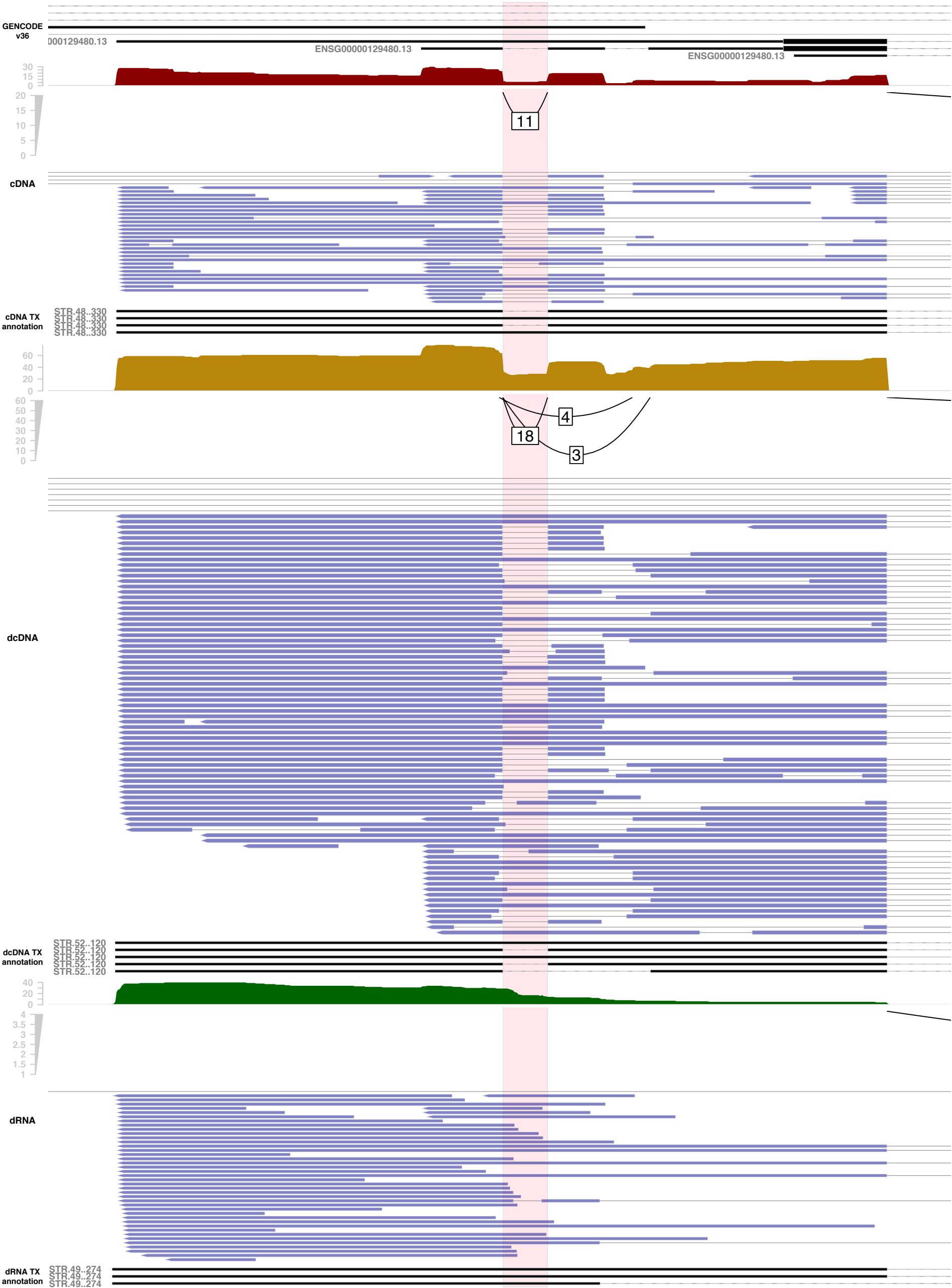
Cell line: Hct116



chr14:31447249-31447389:- RP11-176H8.1,DTD2

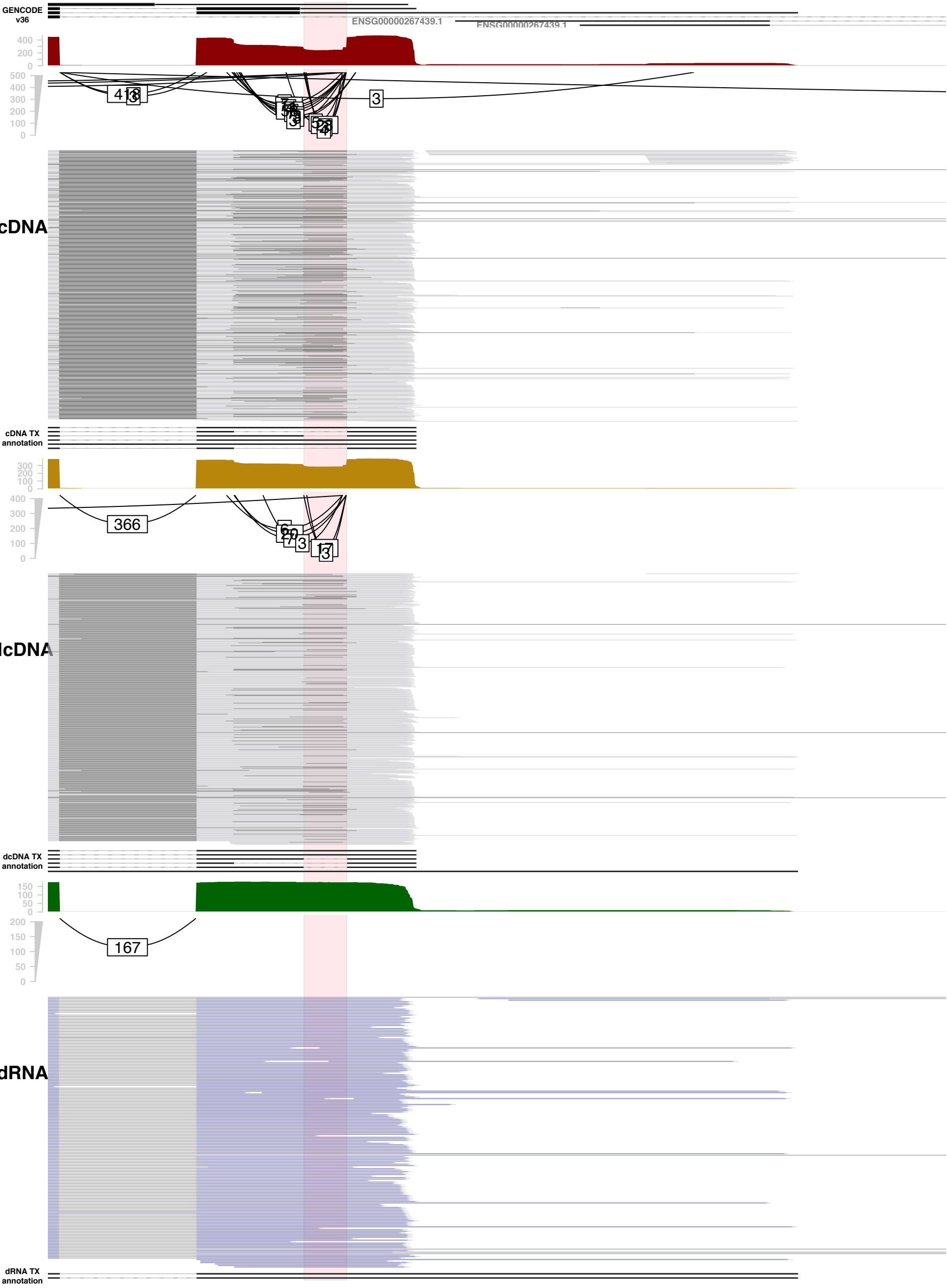
Cell line: Hct116

Direct repeat sequence: CAGCAC



chr19:35746853-35746910:+ PSENEN,AC002398.9

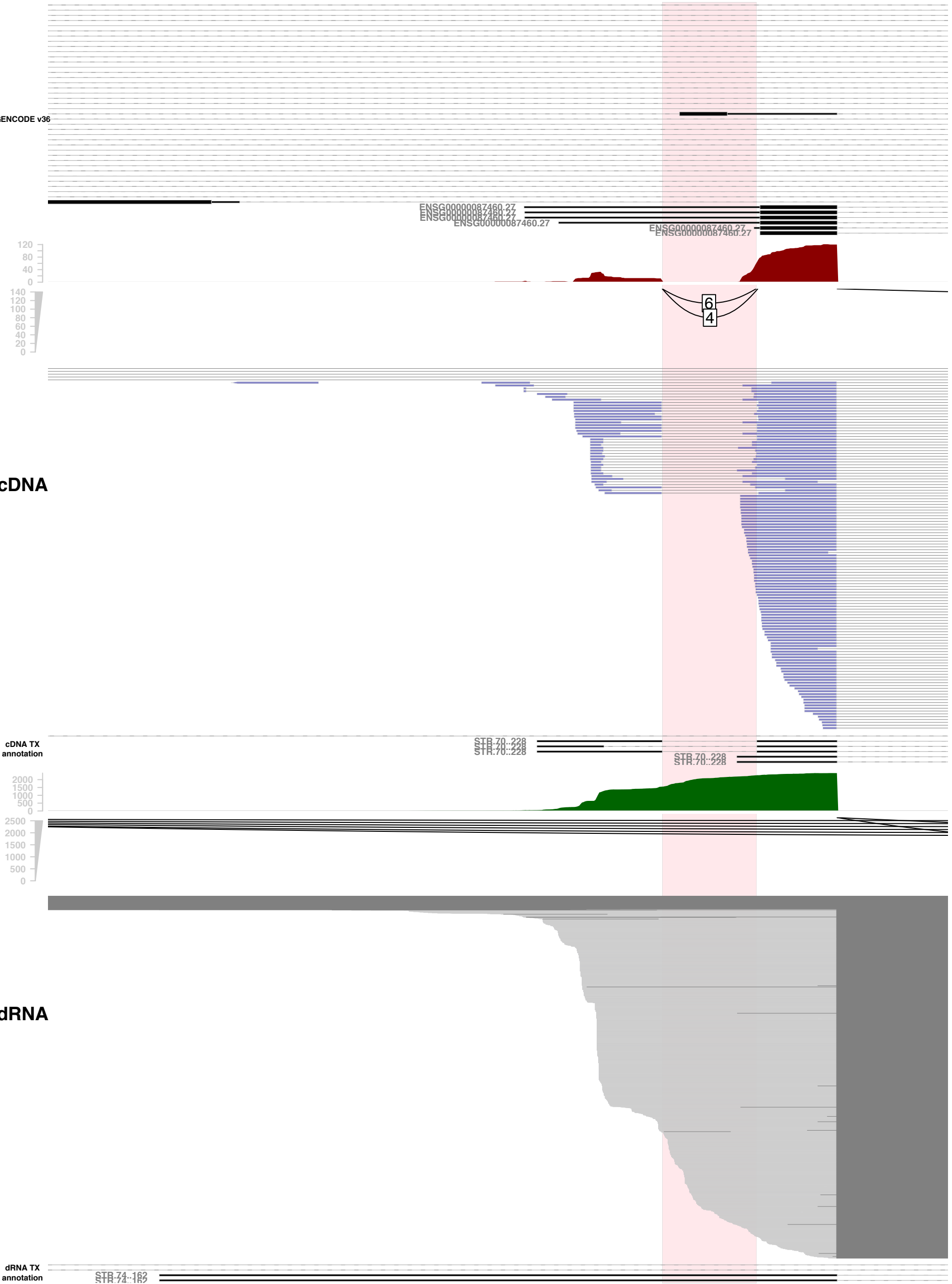
Cell line: Hct116



chr20:58891551-58891720:+ GNAS

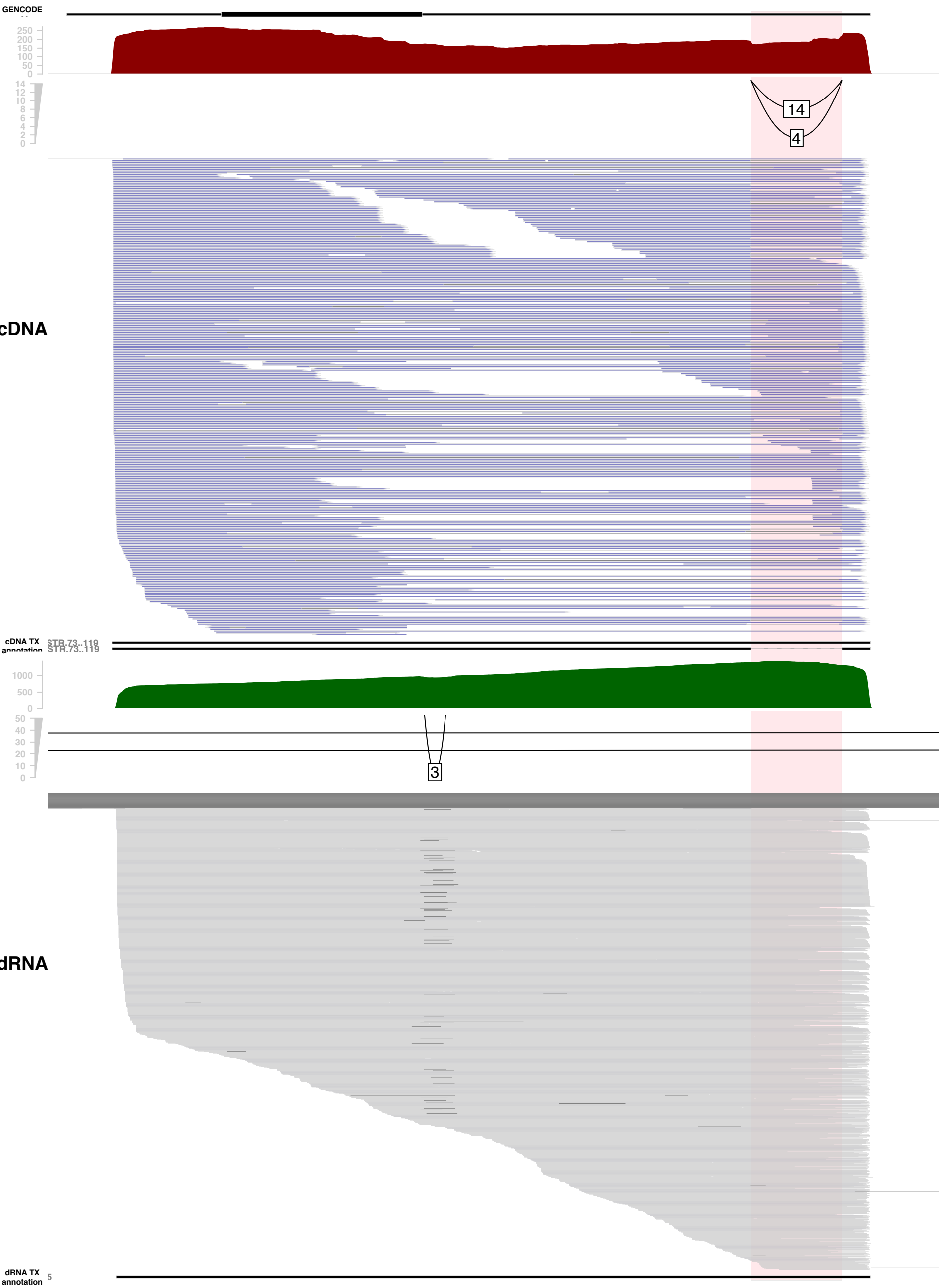
Cell line: Hct116

Direct repeat sequence: CCGCC



chr22:37807089-37807354:+ H1FO

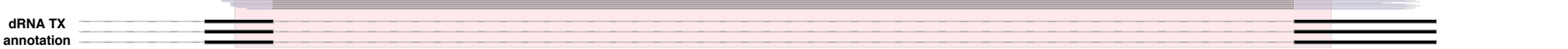
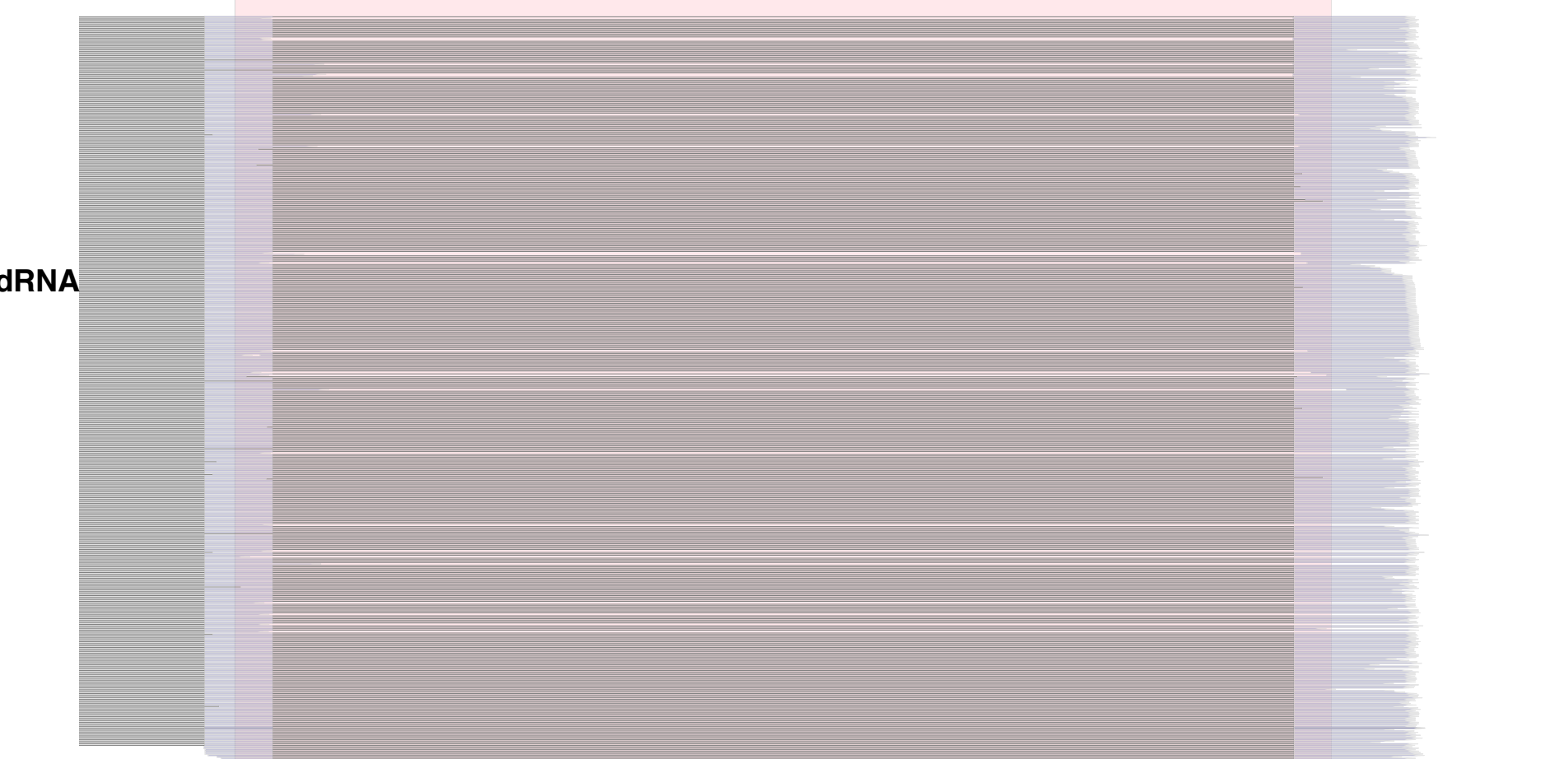
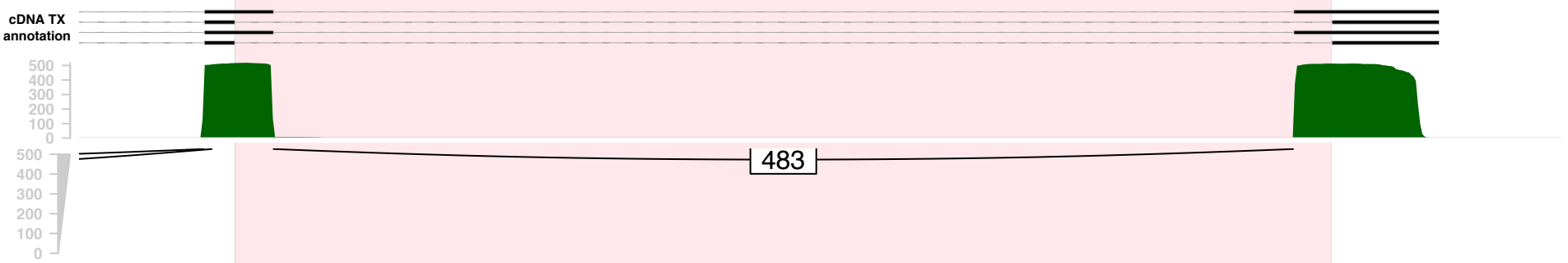
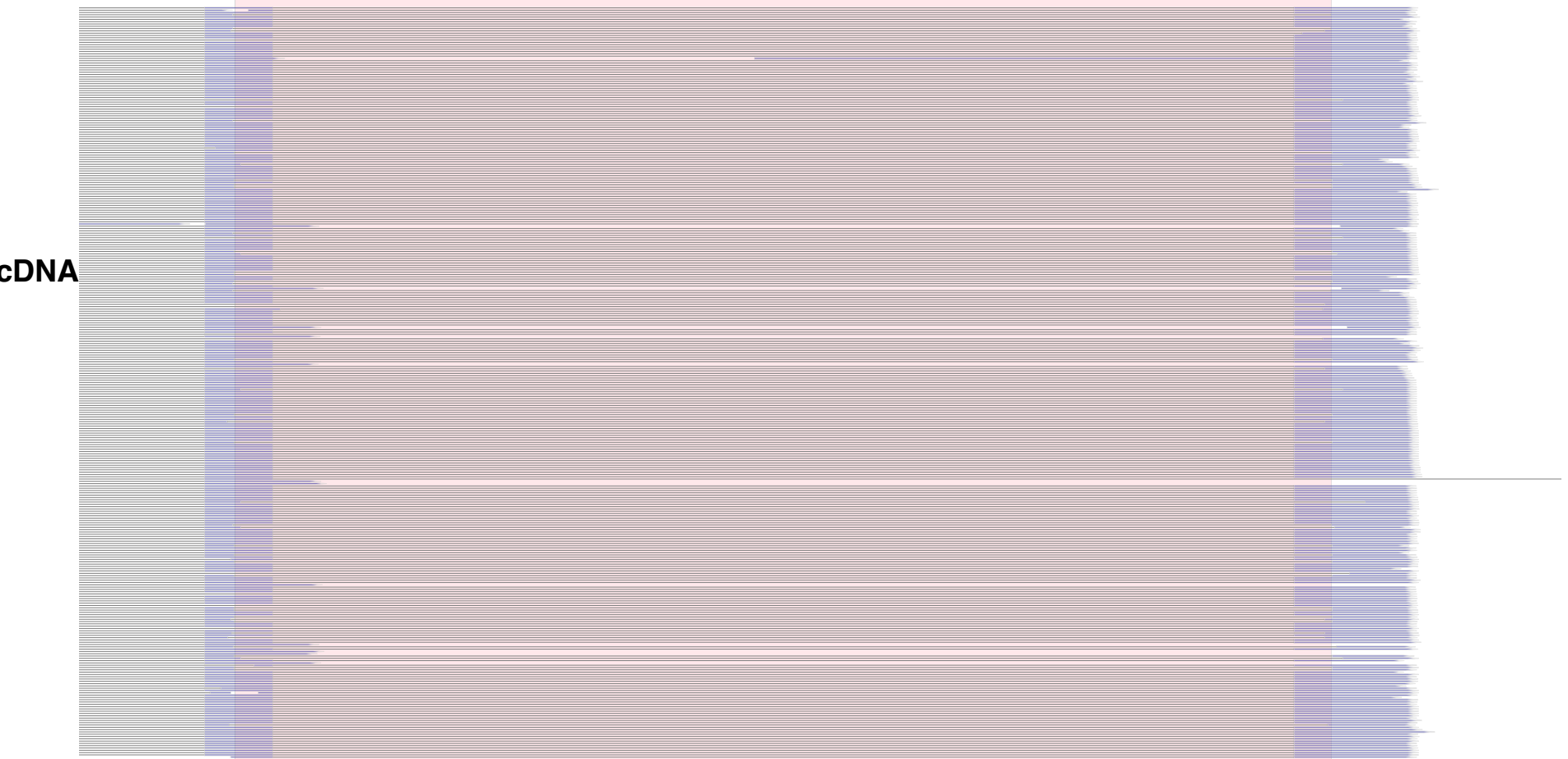
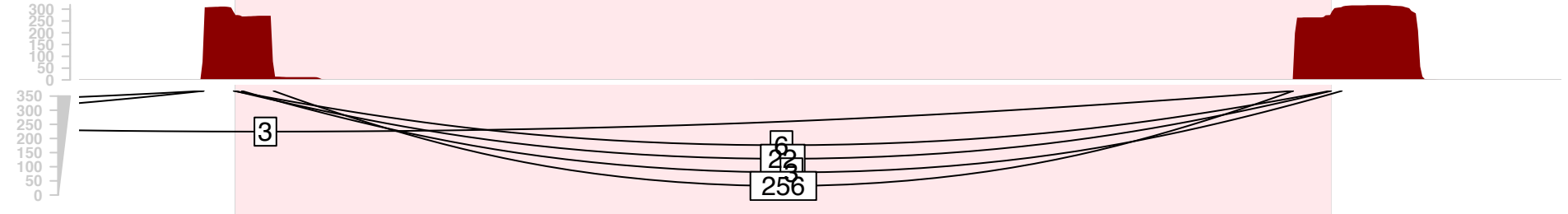
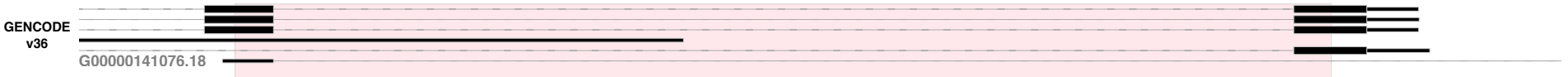
Cell line: Hct116



chr16:69167124-69168881:+ UTP4

Cell line: Hct116

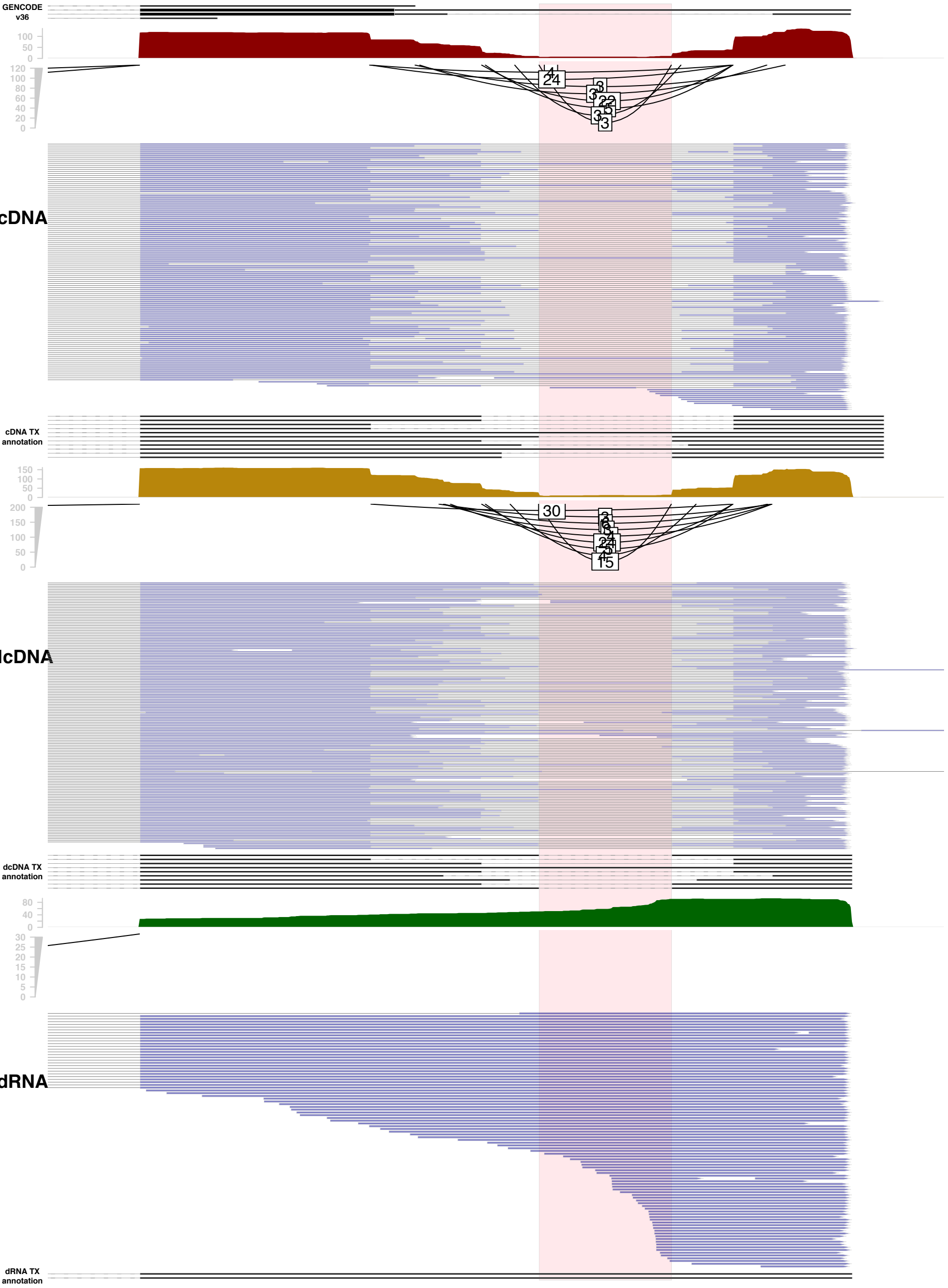
Direct repeat sequence: ATGA



chr1:28335286-28335574:+ MED18

Cell line: Hct116

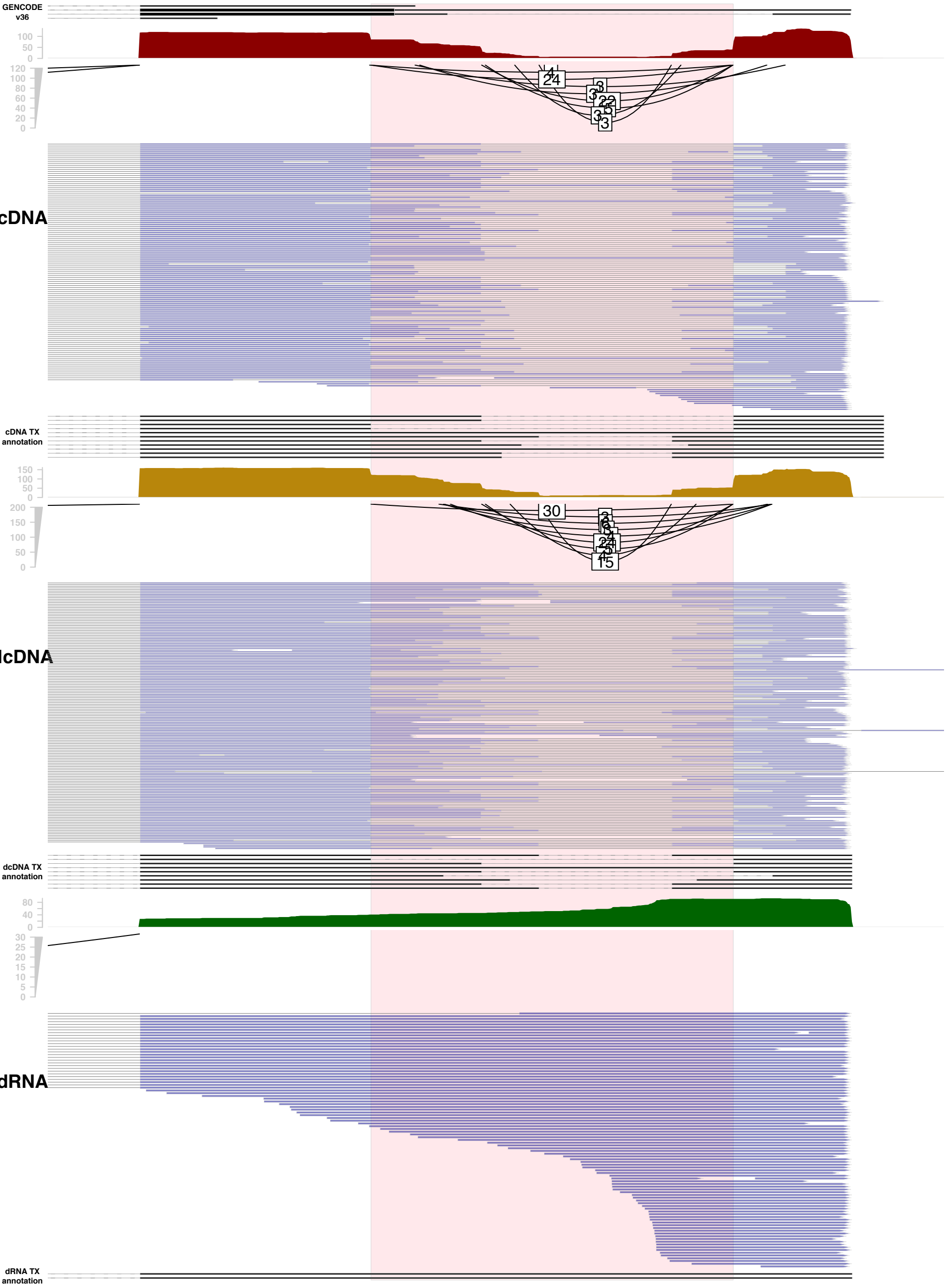
Direct repeat sequence: CCCA



chr1:28334920-28335708:+ MED18

Cell line: Hct116

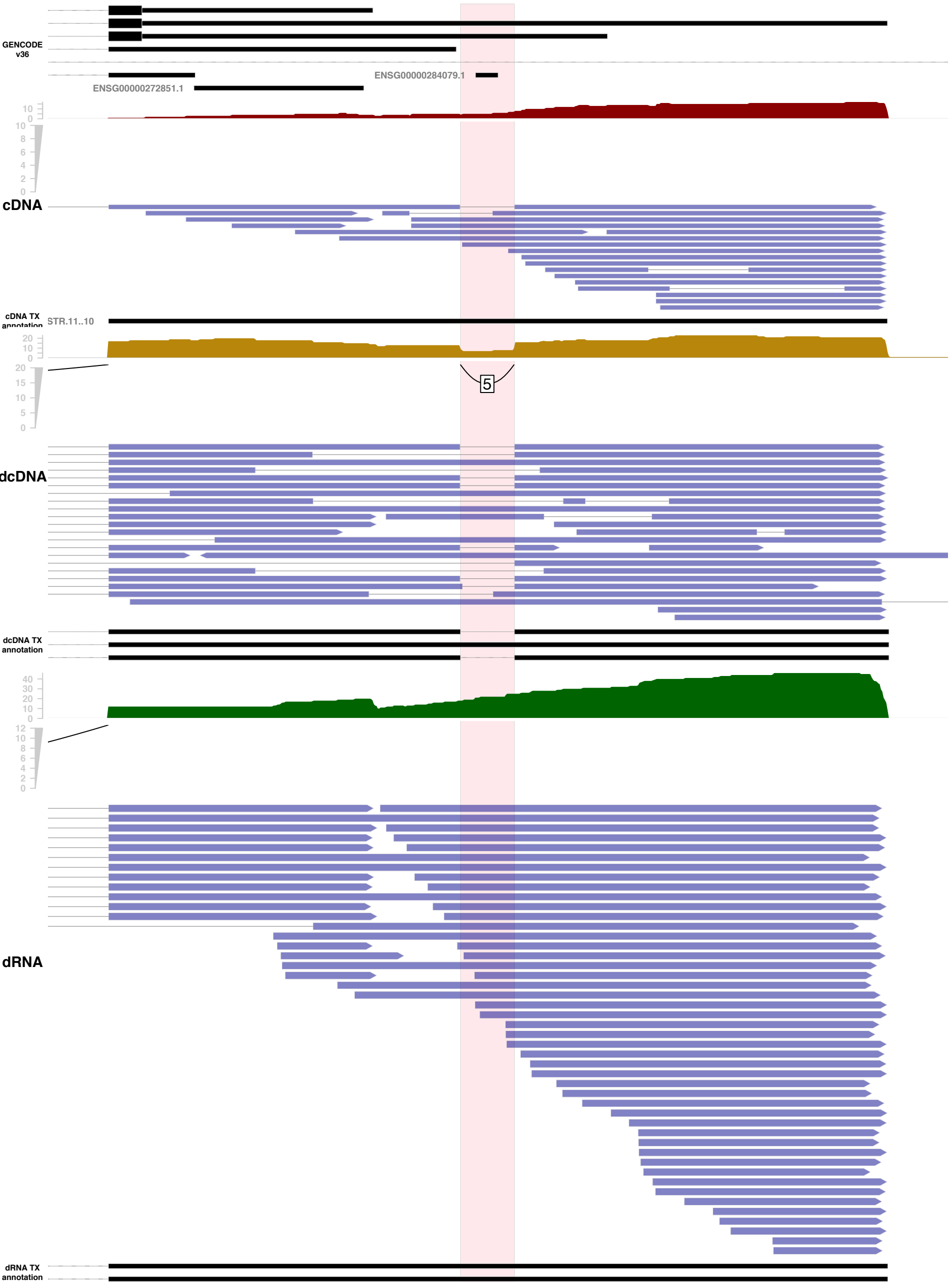
Direct repeat sequence: CAGCTA



chr2:207754757-207754935:+ CCNYL1

Cell line: Hct116

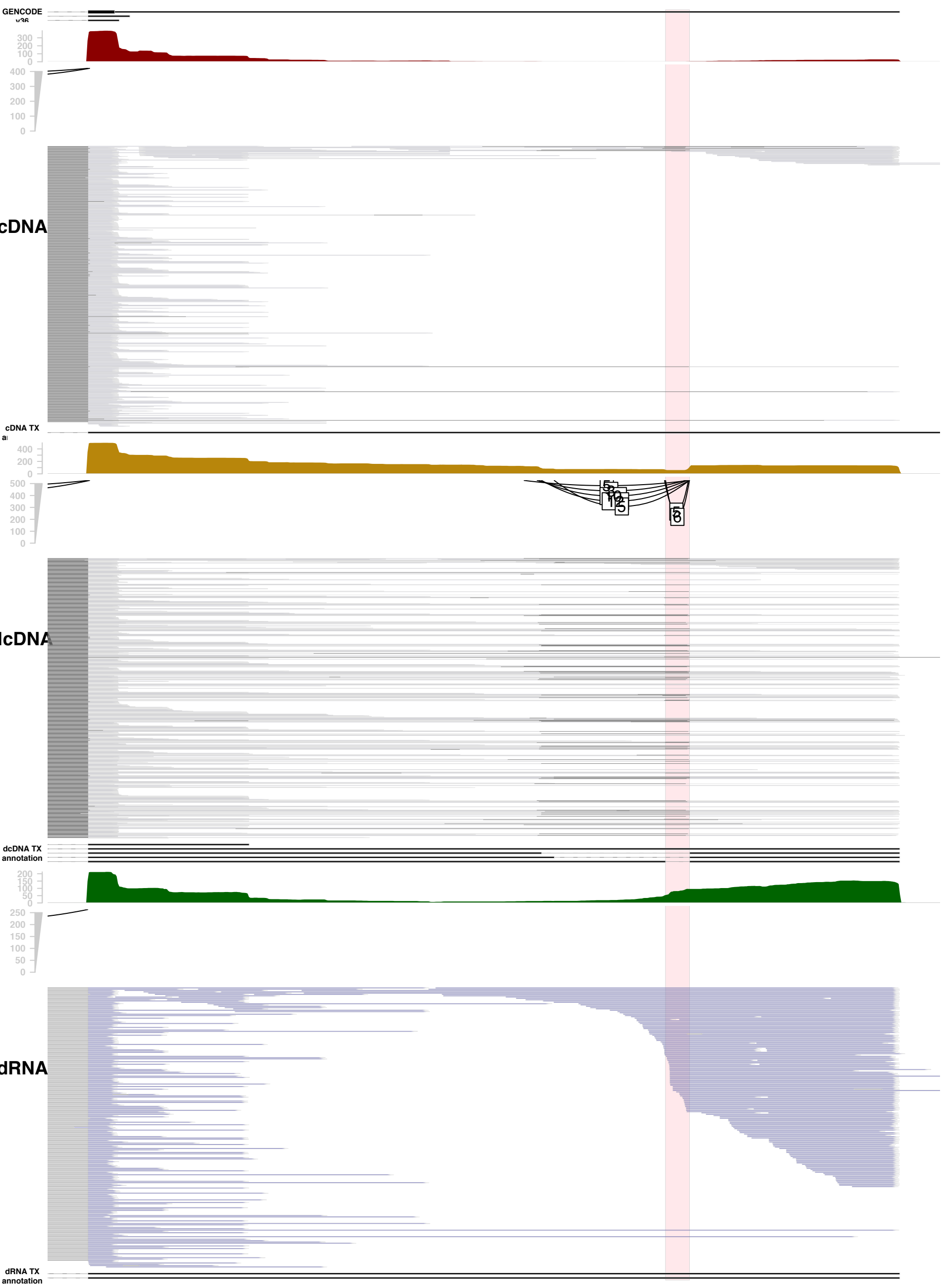
Direct repeat sequence: CAGC



chr4:176331078-176331197:+ SPCS3

Cell line: Hct116

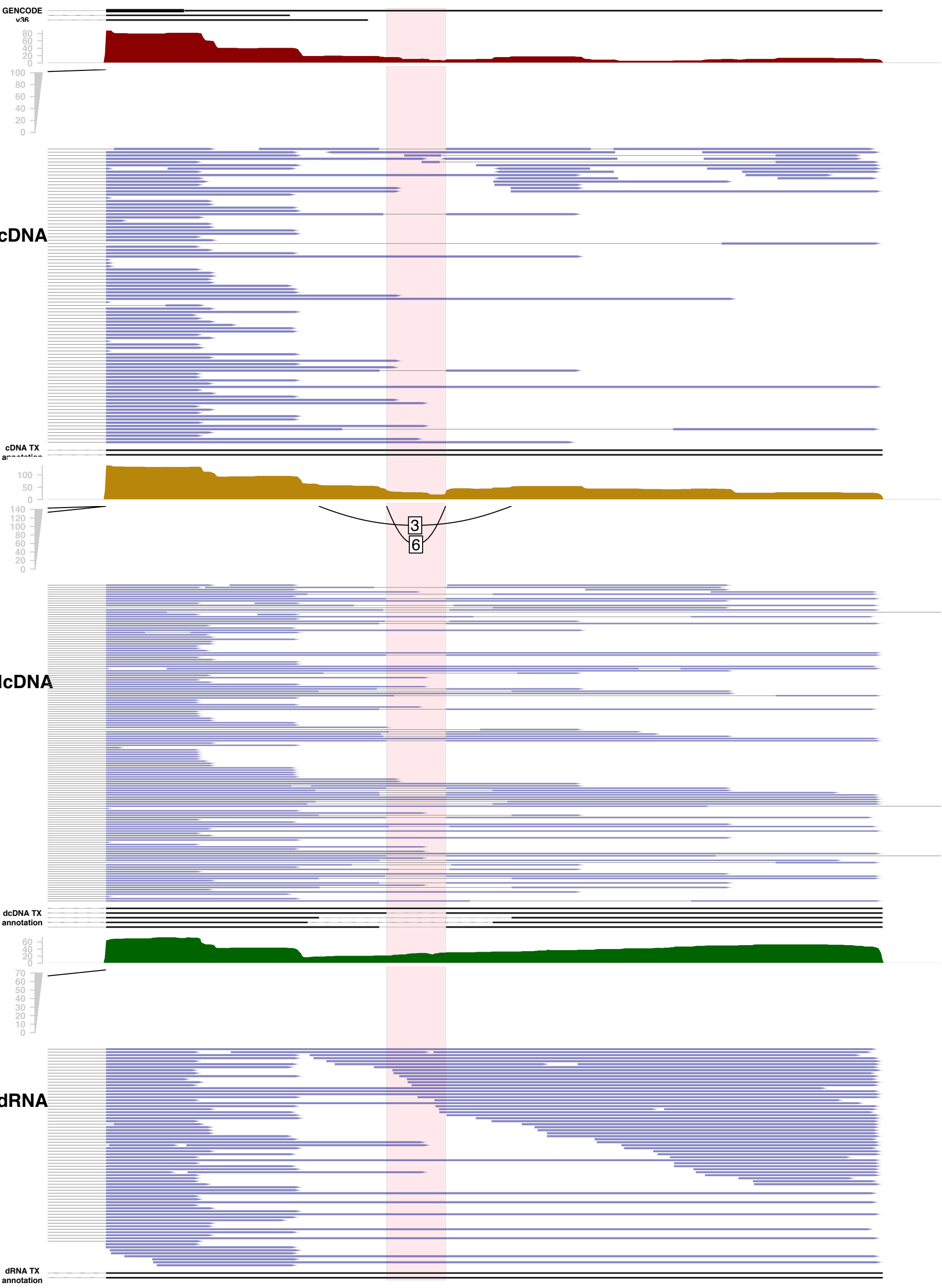
Direct repeat sequence: CAGC



chr5:126625543-126625746:+ PHAX

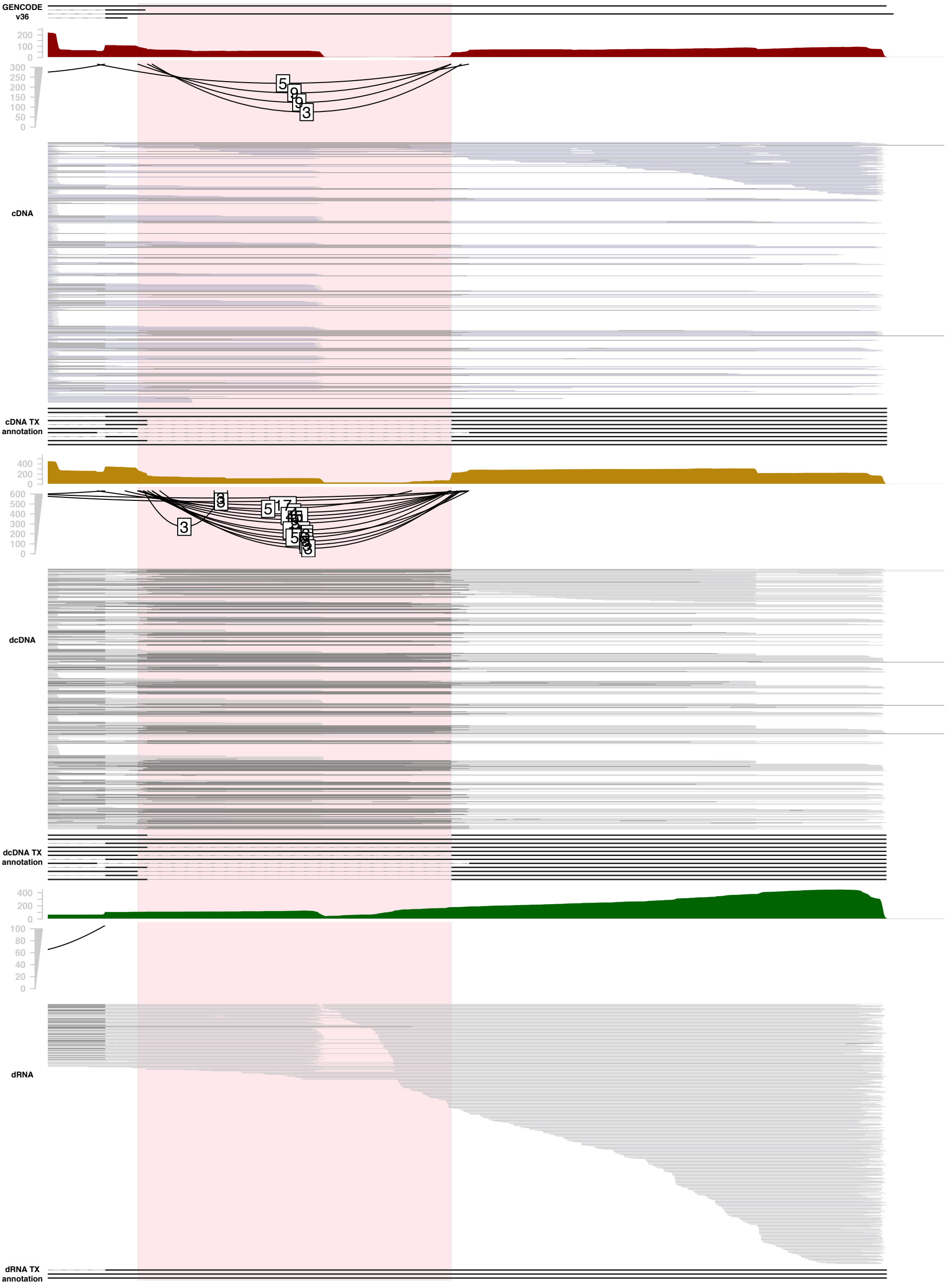
Cell line: Hct116

Direct repeat sequence: GCTG



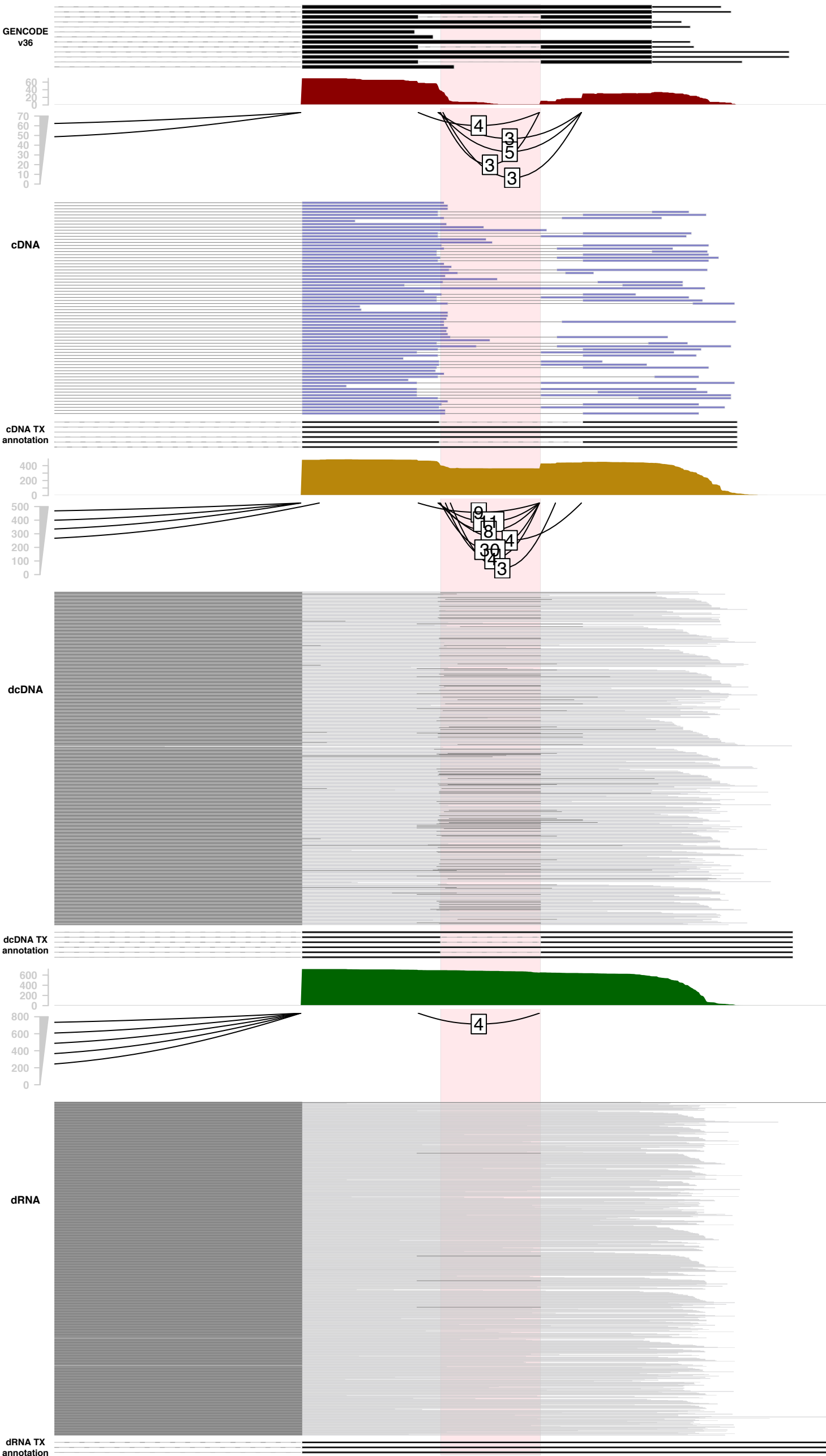
chr6:42887275-42888373:+ RPL7L1

Cell line: Hct116



chr6:170584411-170584491:- PDCD2

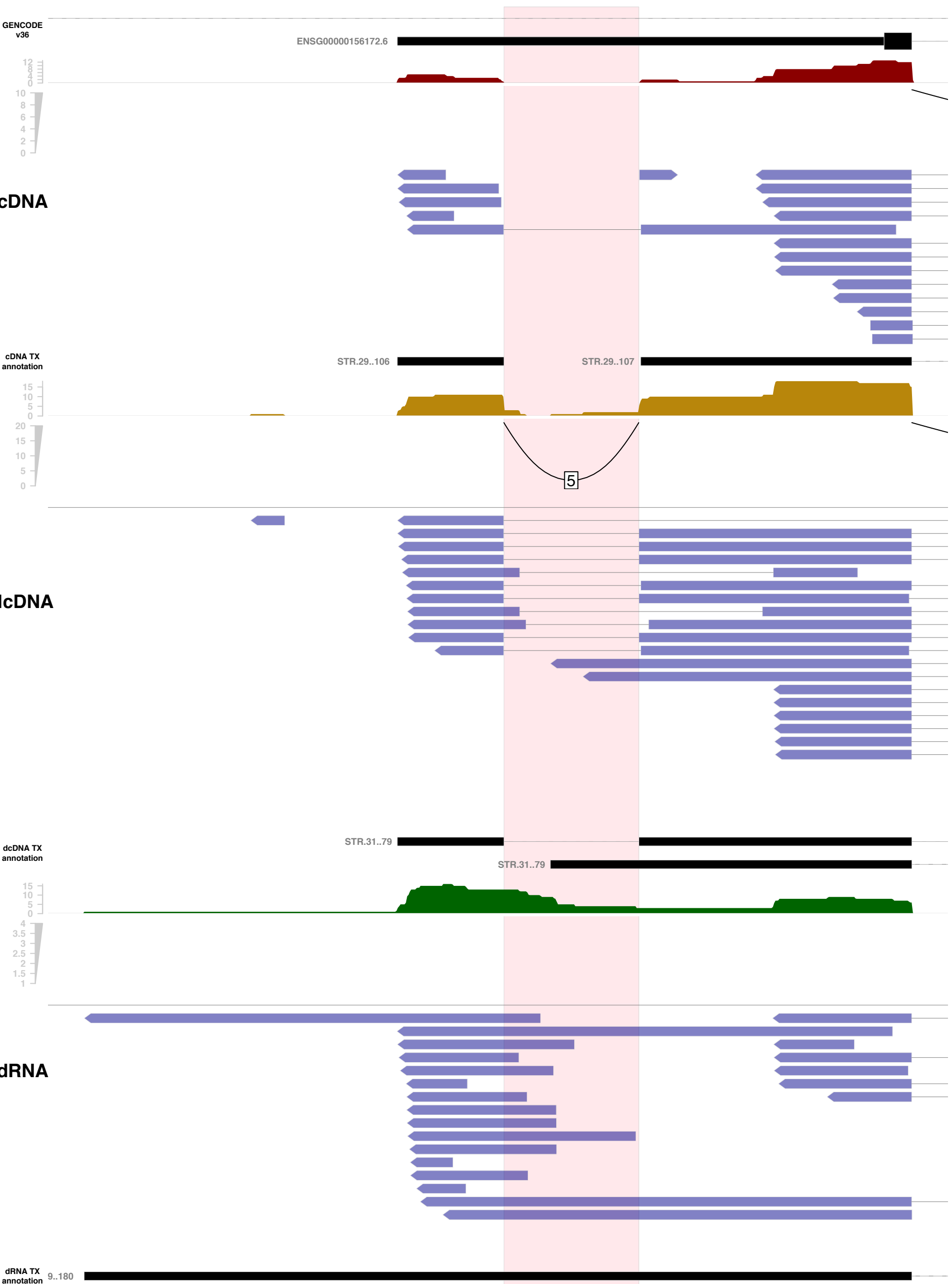
Cell line: Hct116



chr8:95245505-95246254:- C8orf37

Cell line: Hct116

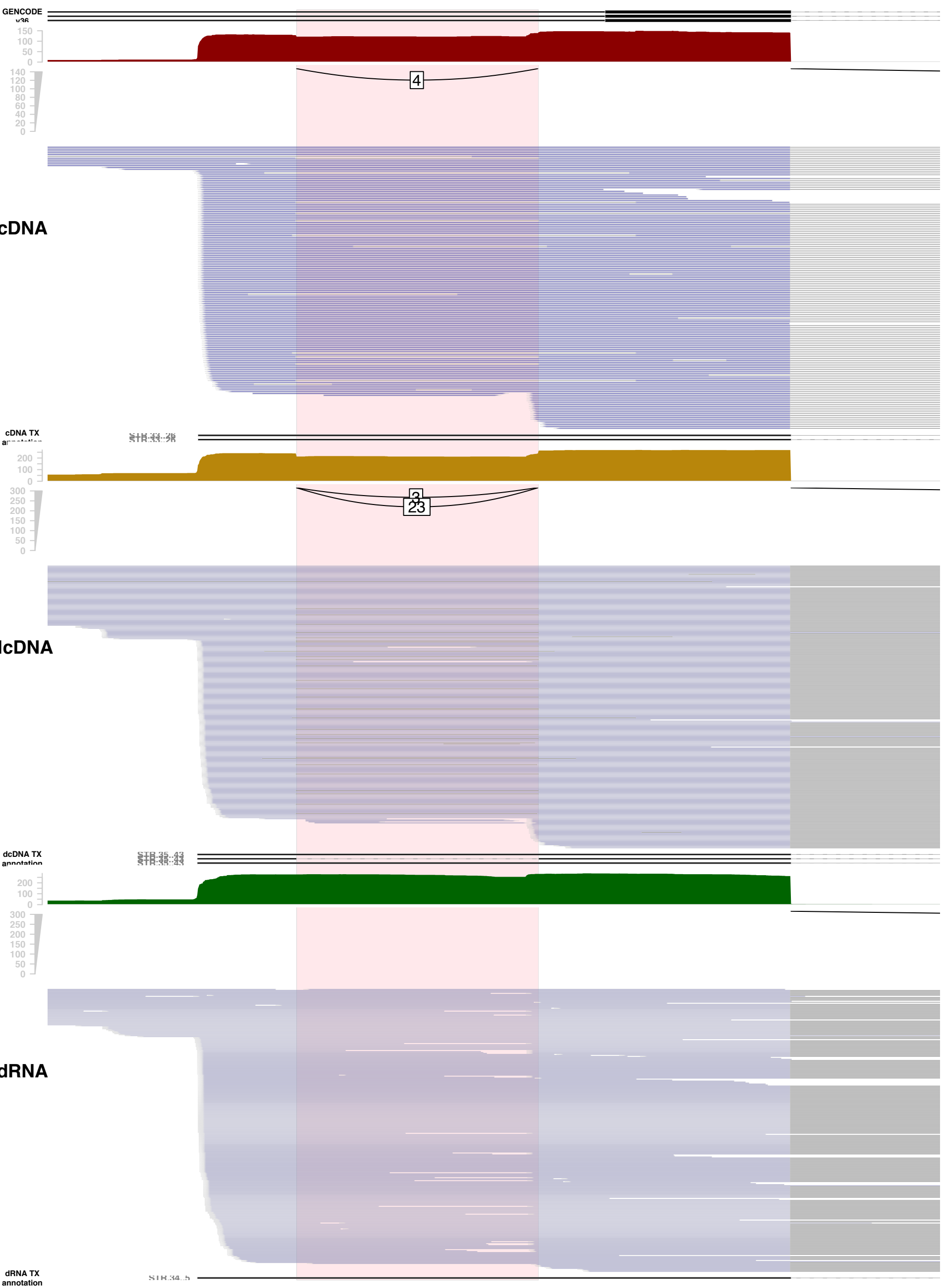
Direct repeat sequence: CAGC



chr9:125149260-125149583:- PPP6C

Cell line: Hct116

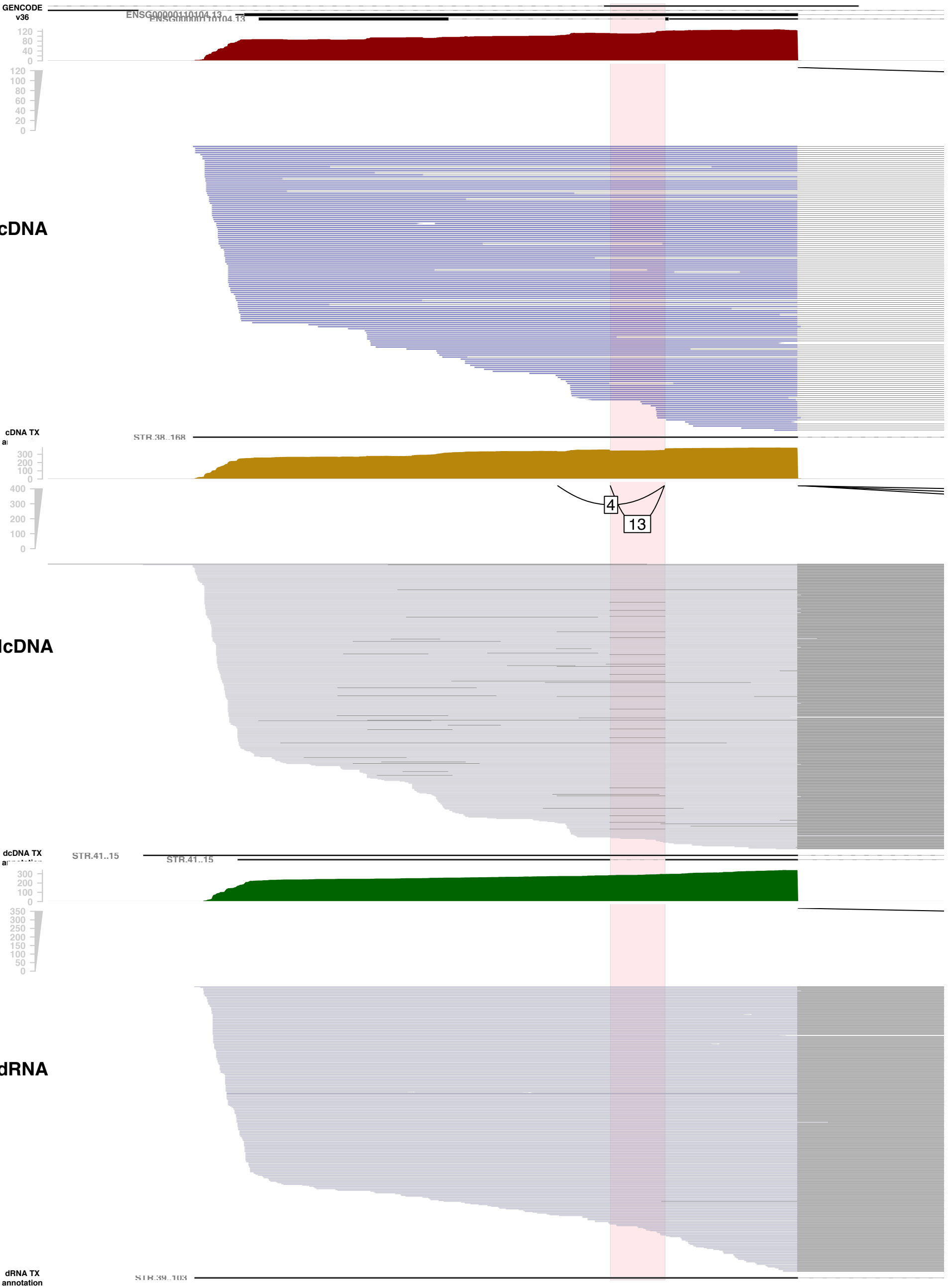
Direct repeat sequence: AGCA



chr11:60842626-60842700:+ CCDC86

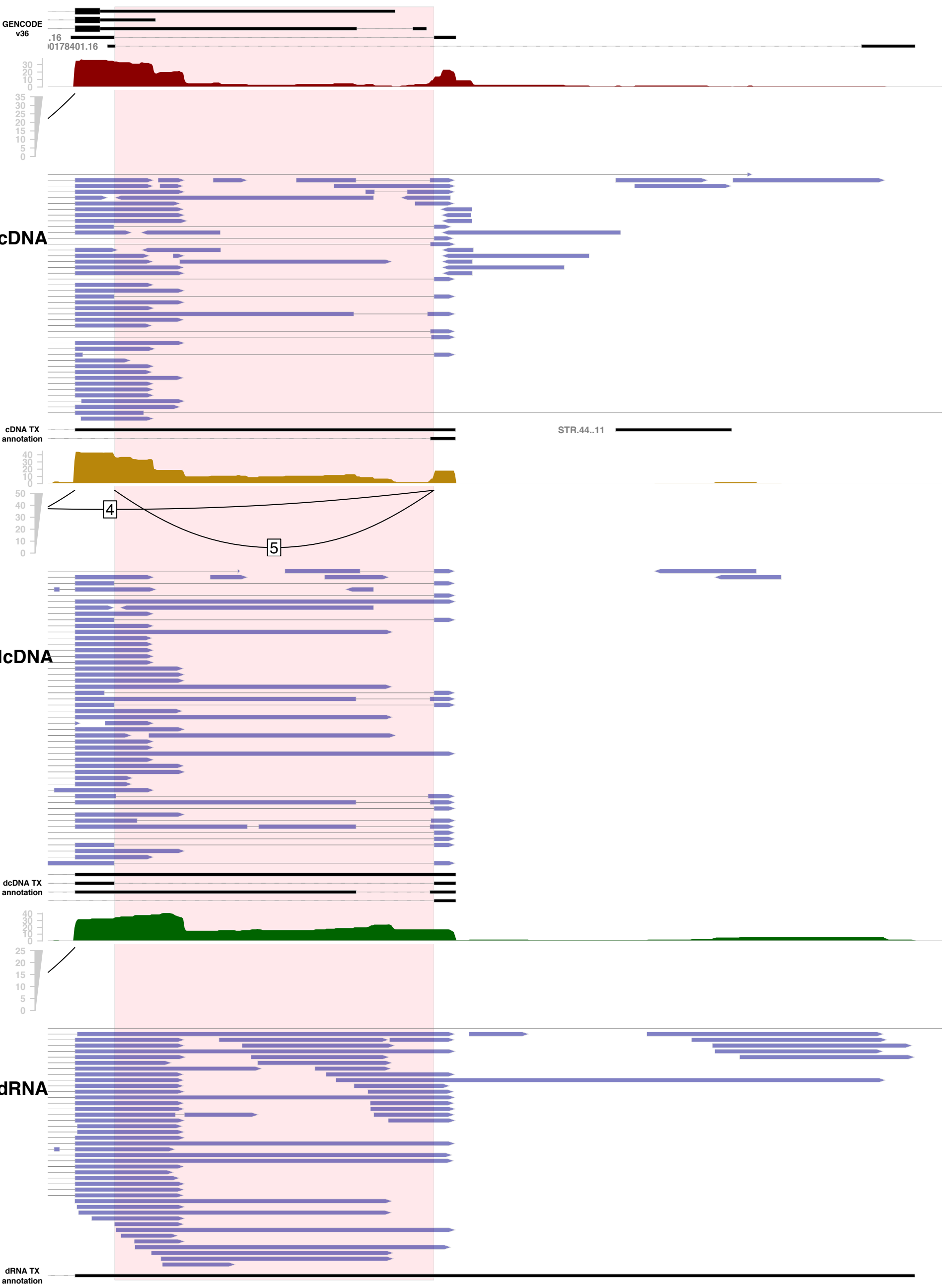
Cell line: Hct116

Direct repeat sequence: GGTCAGCA



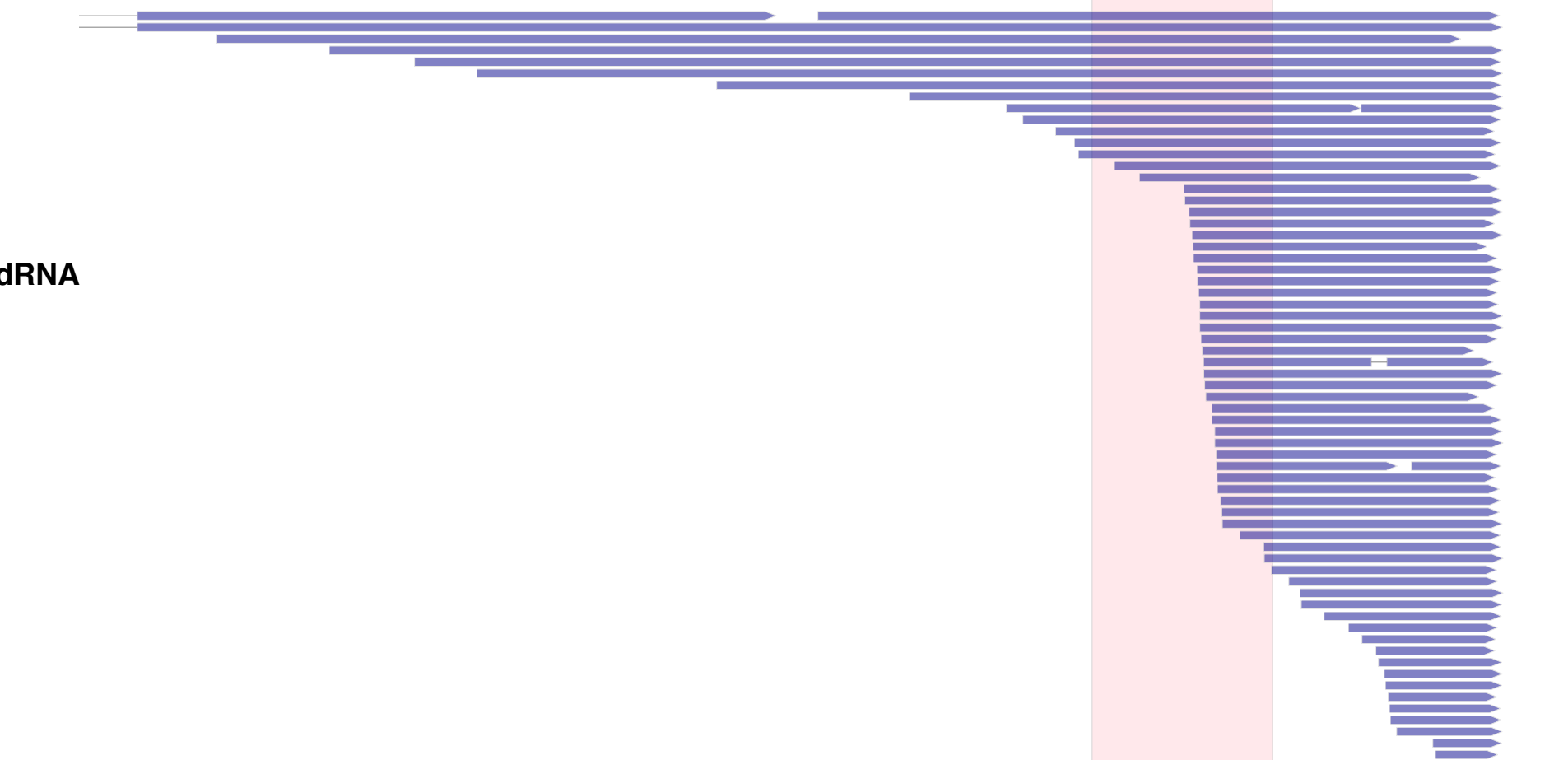
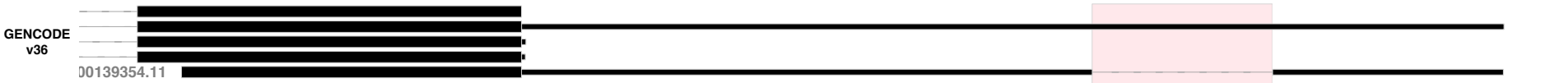
chr12:49351611-49353978:+ DNAJC22

Cell line: Hct116



chr12:100626865-100627488:+ GAS2L3

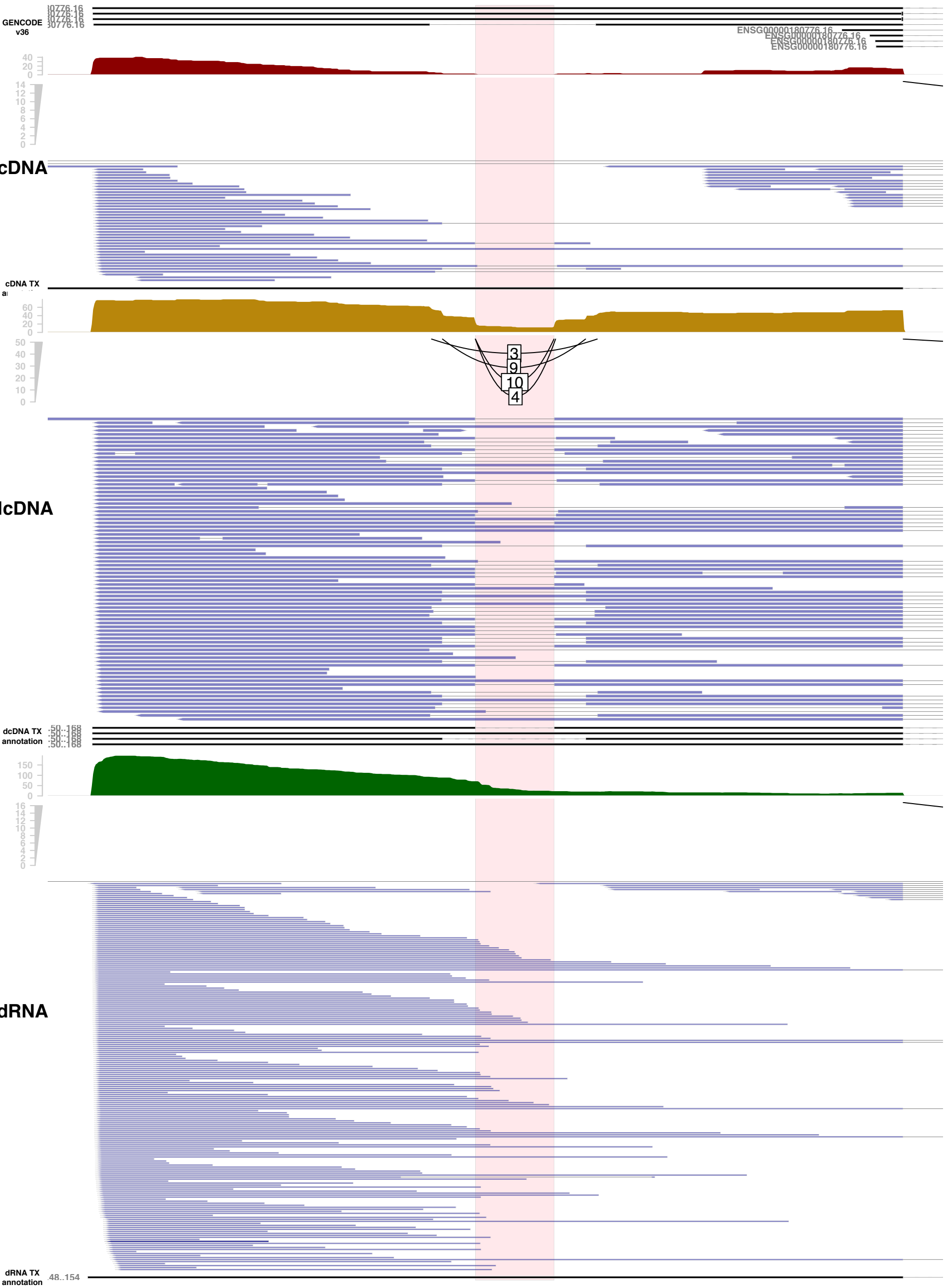
Cell line: Hct116



chr13:21374501-21374897:- ZDHHC20

Cell line: Hct116

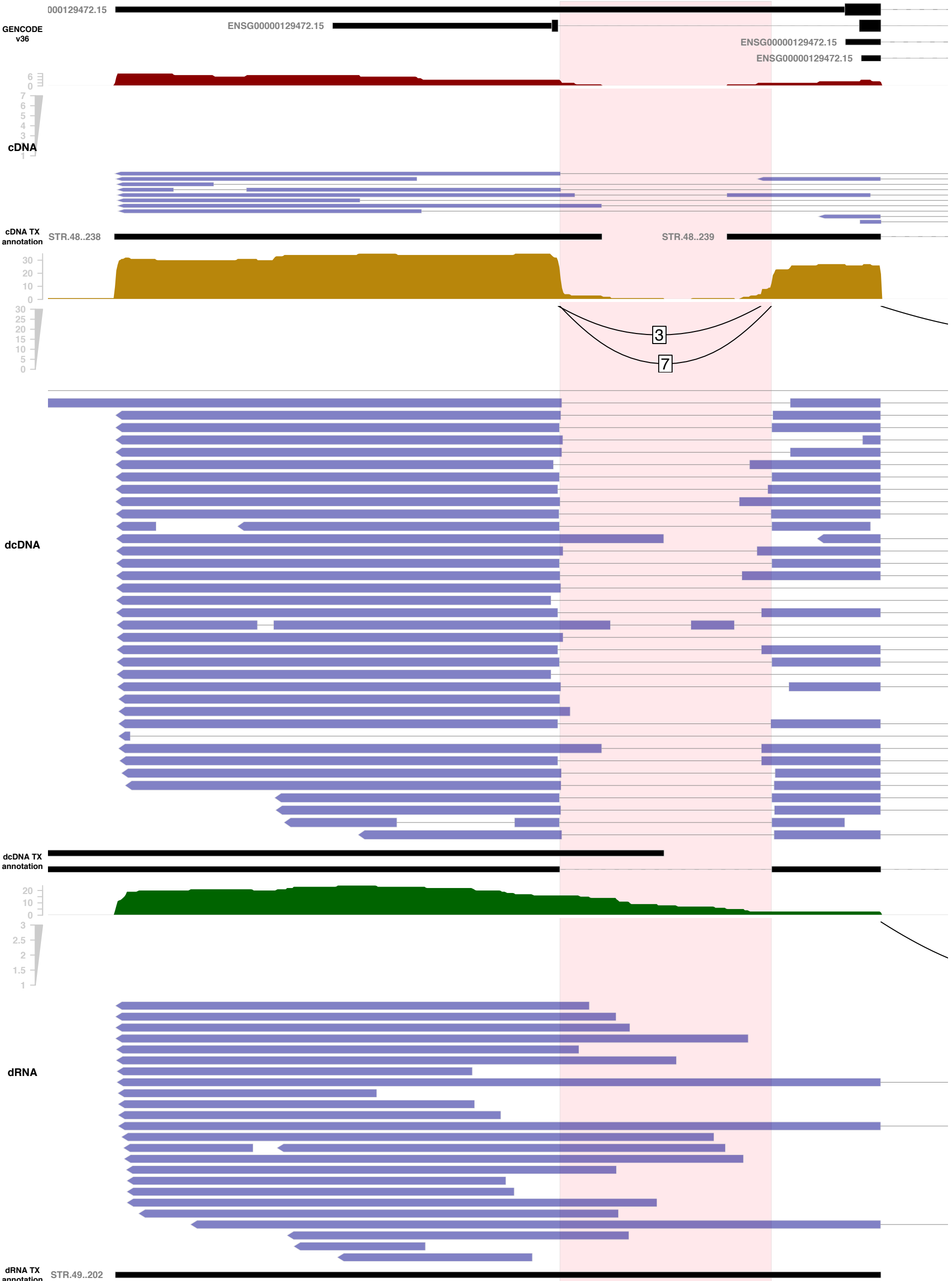
Direct repeat sequence: CAGC



chr14:21460346-21460977:- RAB2B

Cell line: Hct116

Direct repeat sequence: CCTCC

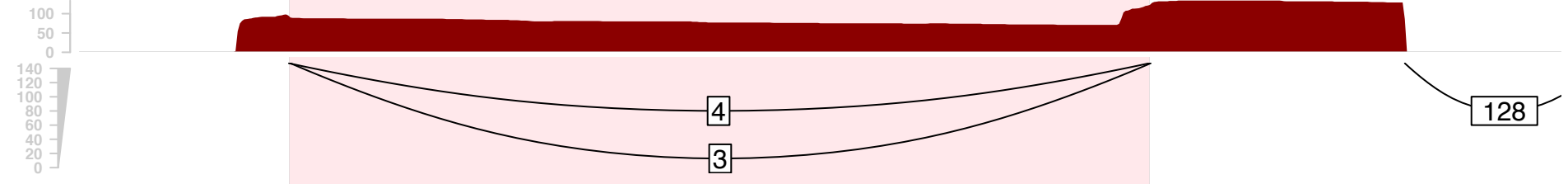


chr15:74843795-74844892:- SCAMP2

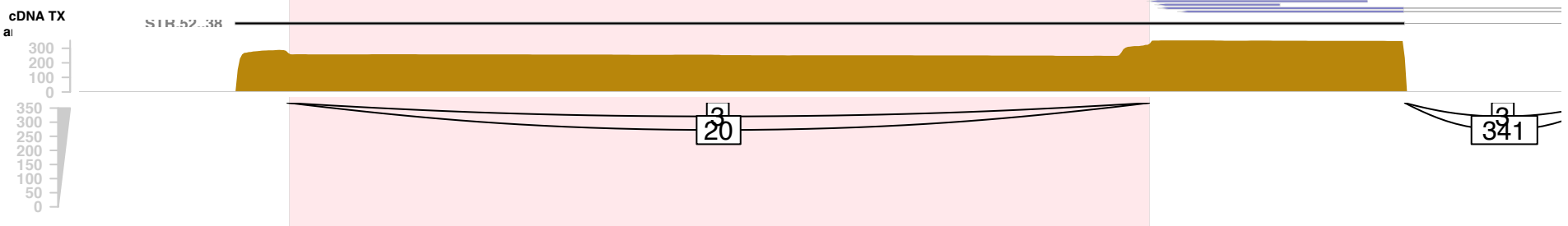
Cell line: Hct116

Direct repeat sequence: CCCCTCTATGTACAAA

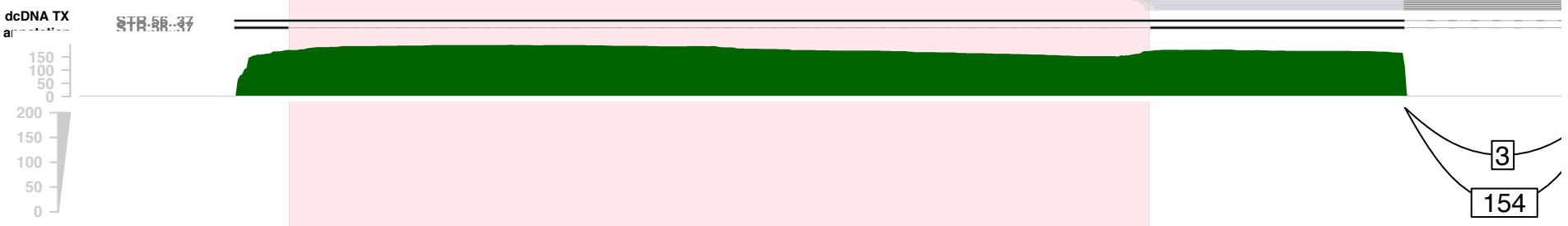
GENCODE v36
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cDNA



cDNA

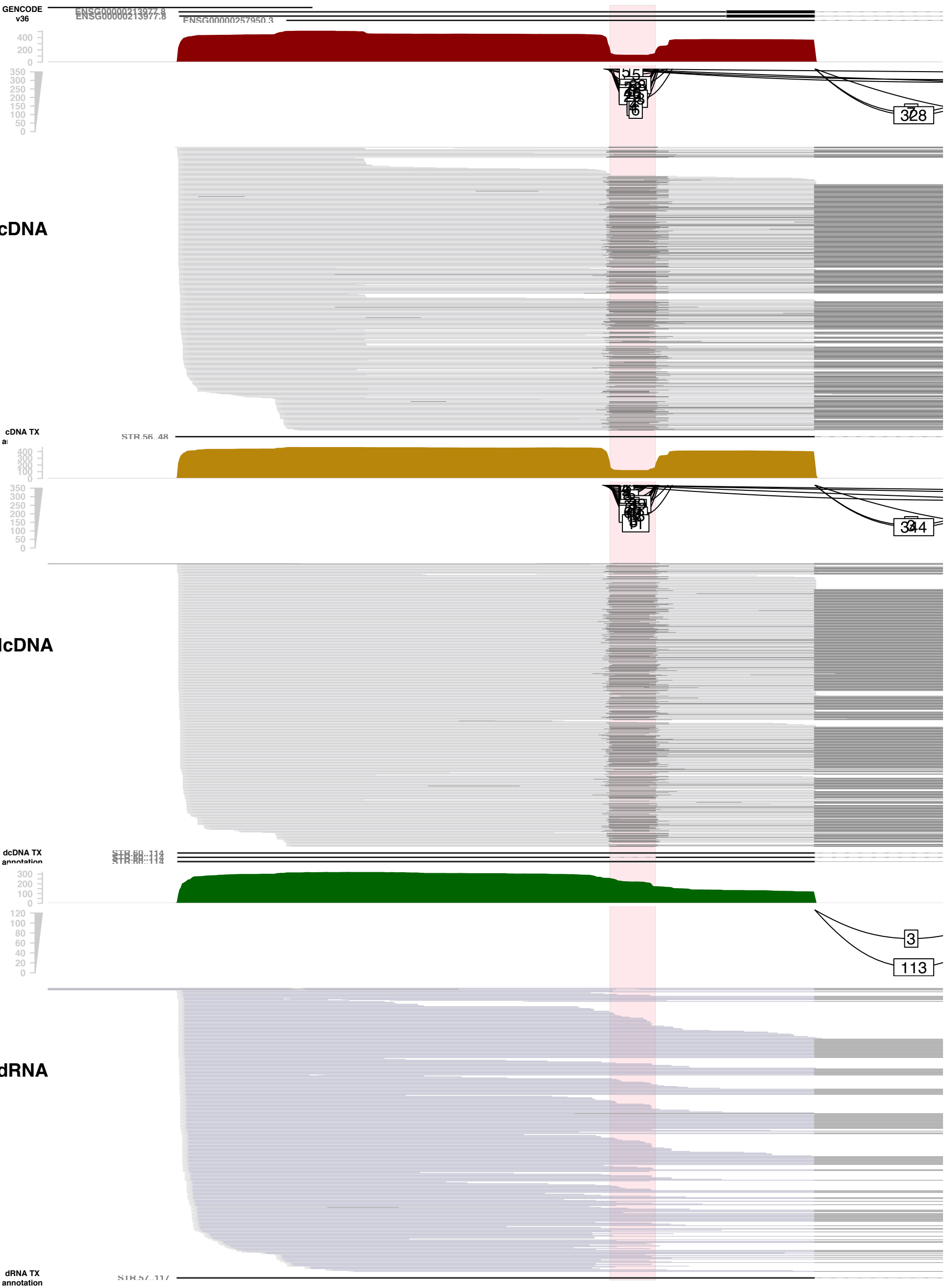


dRNA

dRNA TX annotation
STR:53..40

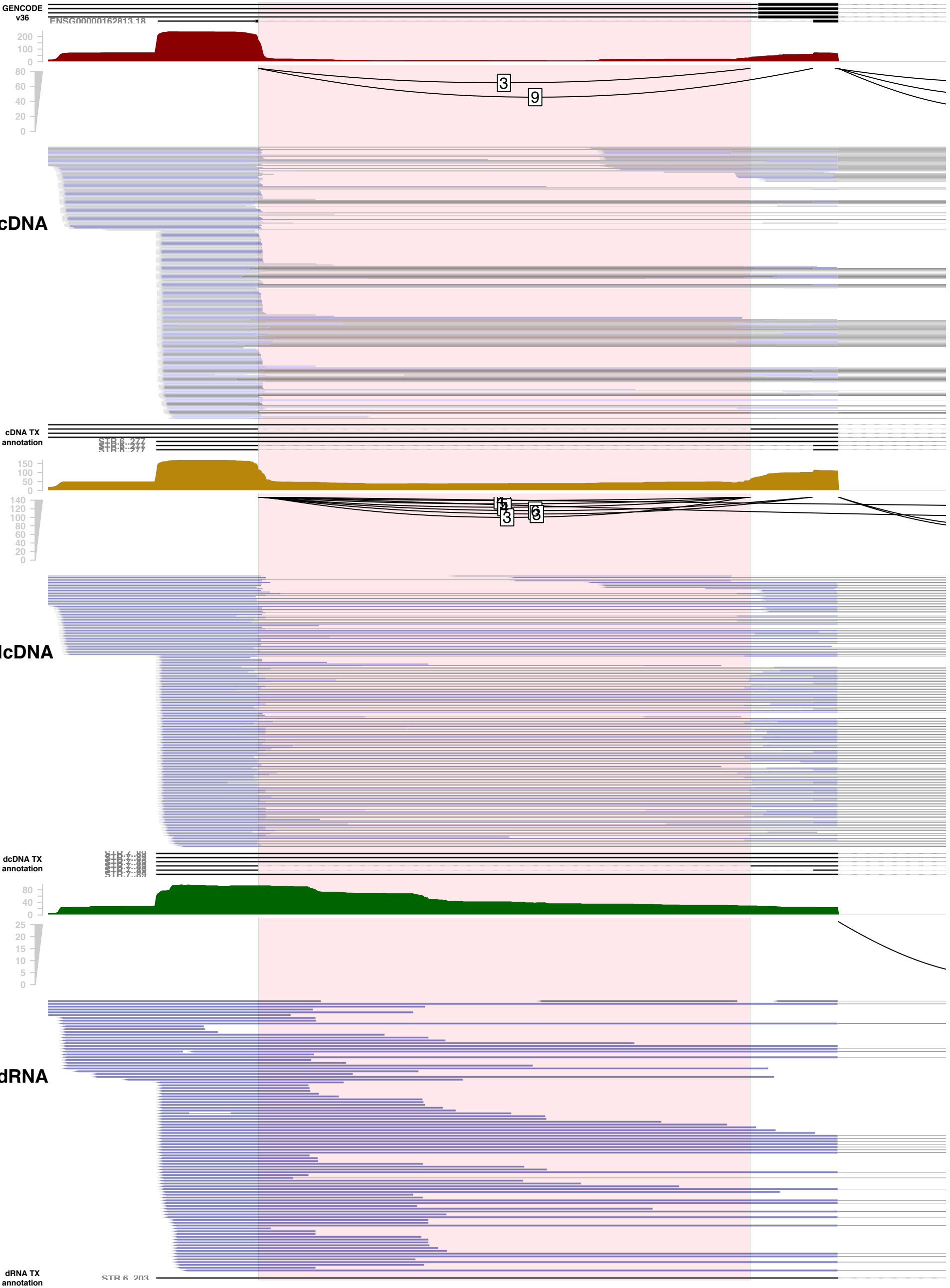
chr17:3663567-3663637:- TAX1BP3,P2RX5-TAX1BP3

Cell line: Hct116



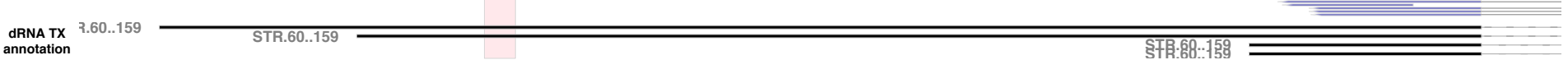
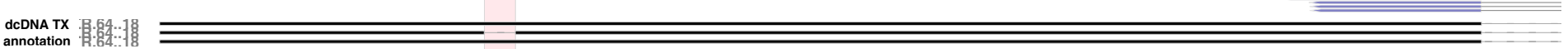
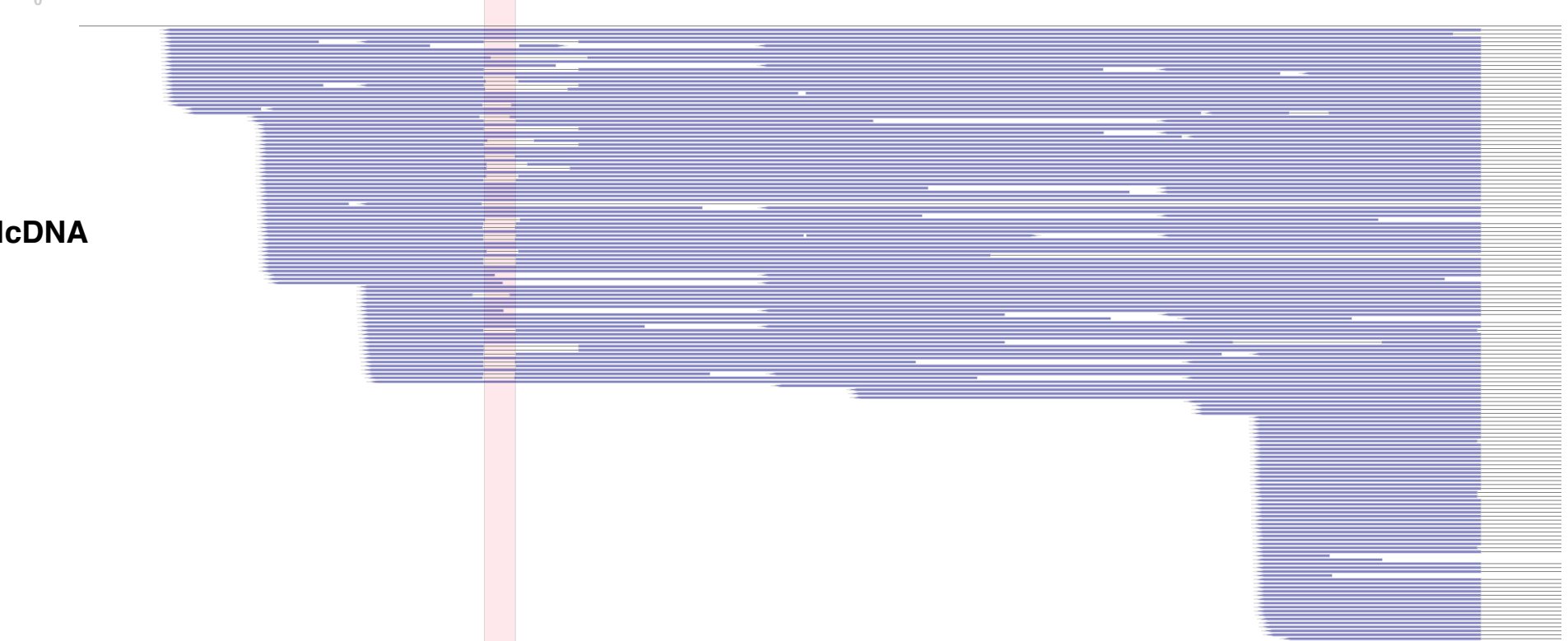
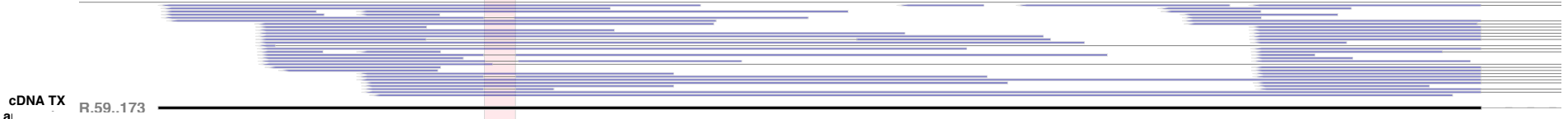
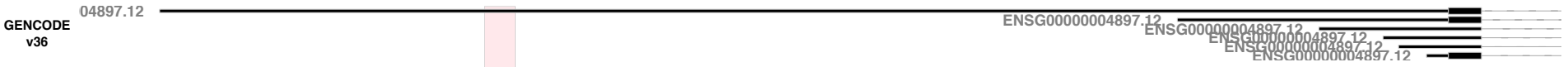
chr1:220057918-220058829:- BPNT1

Cell line: Hct116



chr17:47118517-47118594:- CDC27

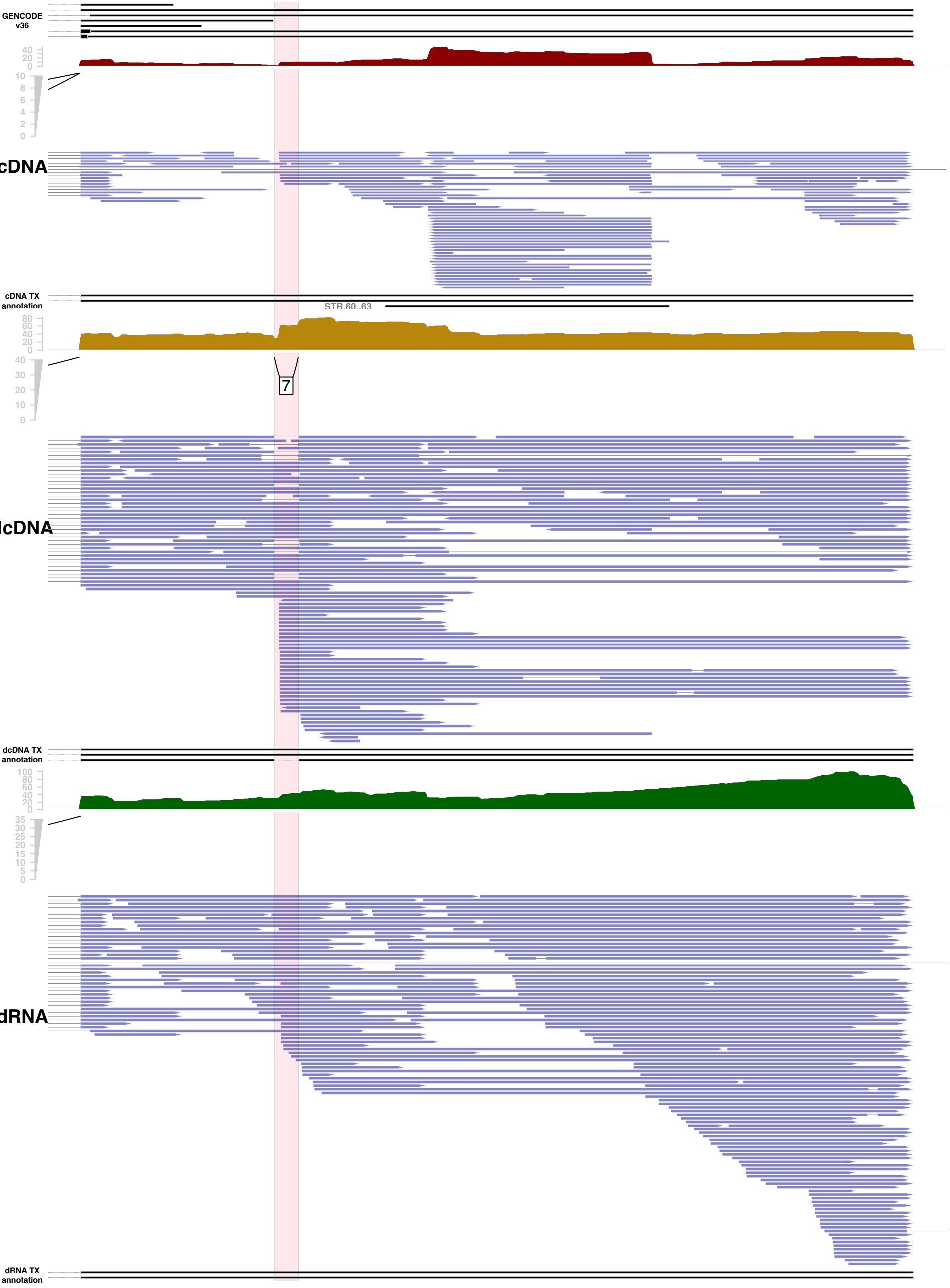
Cell line: Hct116



chr17:57680745-57680893:+ MSI2

Cell line: Hct116

Direct repeat sequence: CCTG



chr20:45883263-45884986:+ ZSWIM1

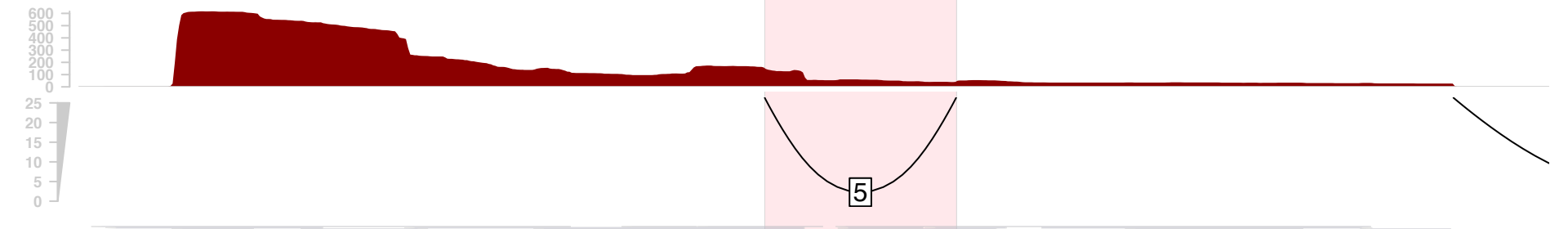
Cell line: Hct116

Direct repeat sequence: CTCCAGCC

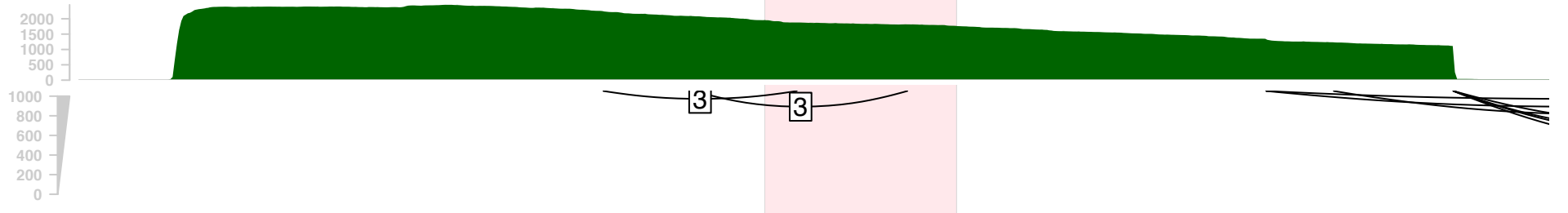


chr1:8012958-8013358:- ERRFI1
Cell line: HepG2
Direct repeat sequence: GGGAAGC

GENCODE 0116285.13 v36
ENSG00000116285.13
ENSG00000116285.13
ENSG00000116285.13



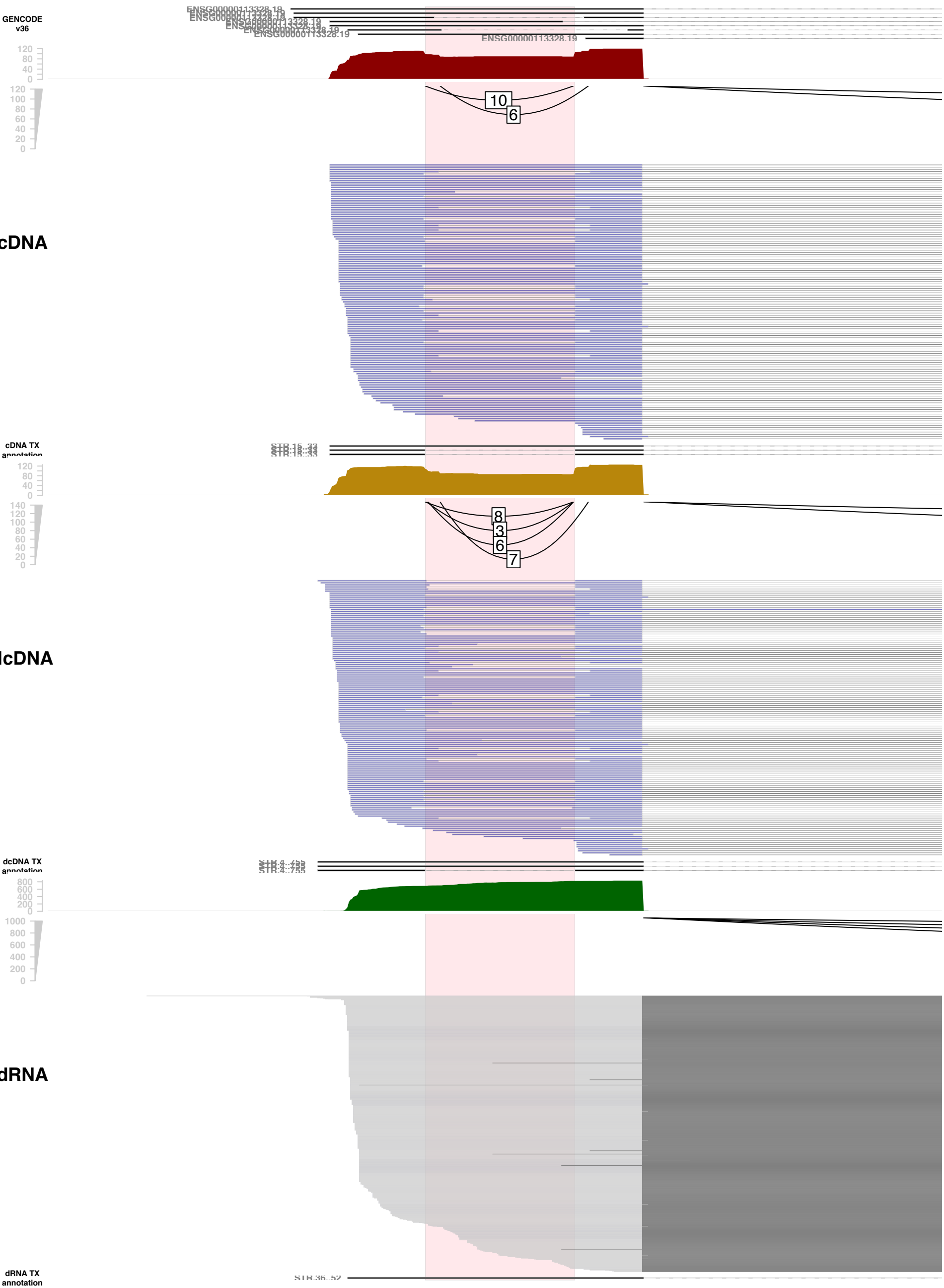
cDNA TX annotation STR:0:116 STR:0:116



dRNA TX annotation STR:0:133 STR:0:133

chr5:163437659-163437758:+ CCNG1

Cell line: HepG2



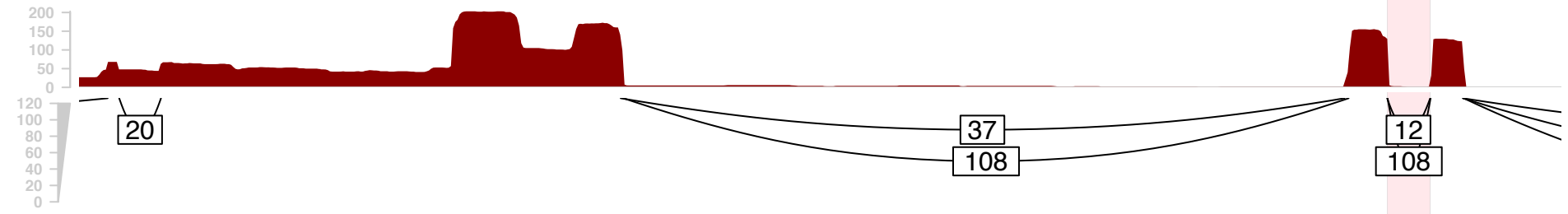
chr12:75501816-75501921:+ GLIPR1

Cell line: HepG2

GENCODE v36

ENSG00000111615.14

ENSG00000111615.14



20

37

12

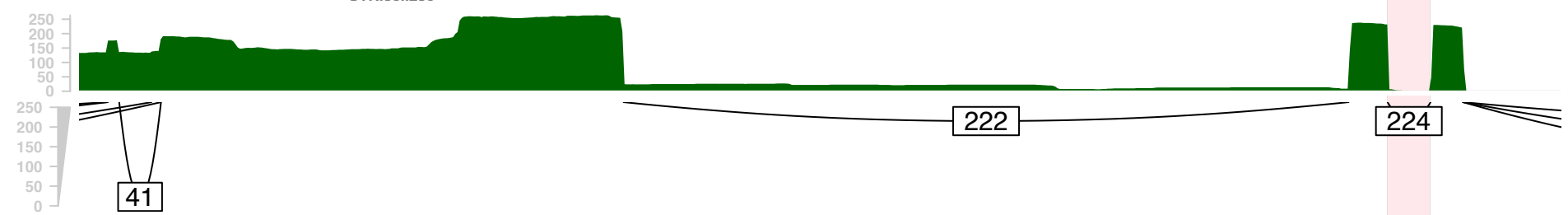
108

108

cDNA

cDNA TX annotation

STR.30..239



41

222

224

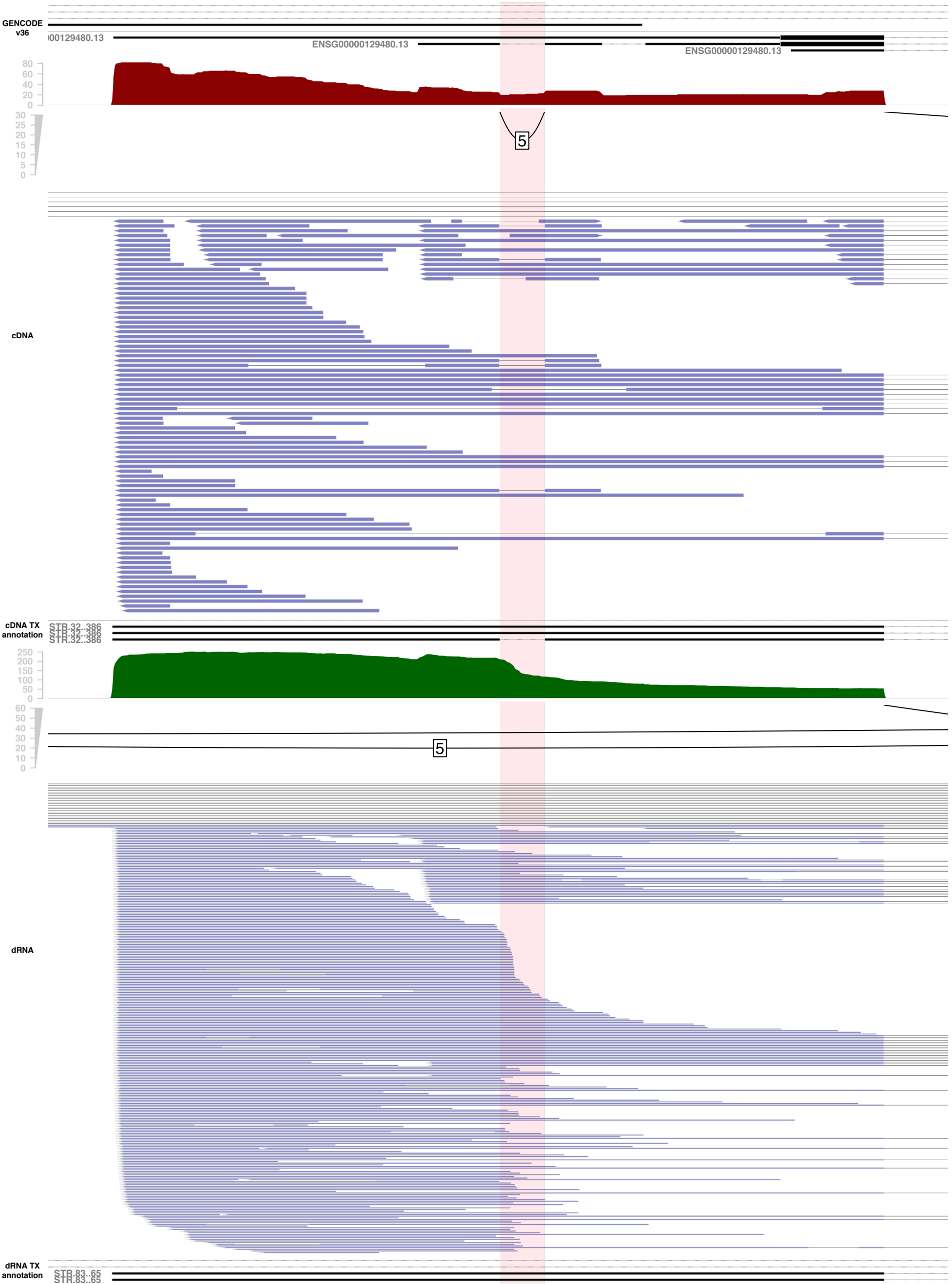
dRNA

dRNA TX annotation

chr14:31447249-31447389:- RP11-176H8.1,DTD2

Cell line: HepG2

Direct repeat sequence: CAGCAC



chr17:3663563-3663657:- TAX1BP3,P2RX5-TAX1BP3

Cell line: HepG2

Direct repeat sequence: GACCG

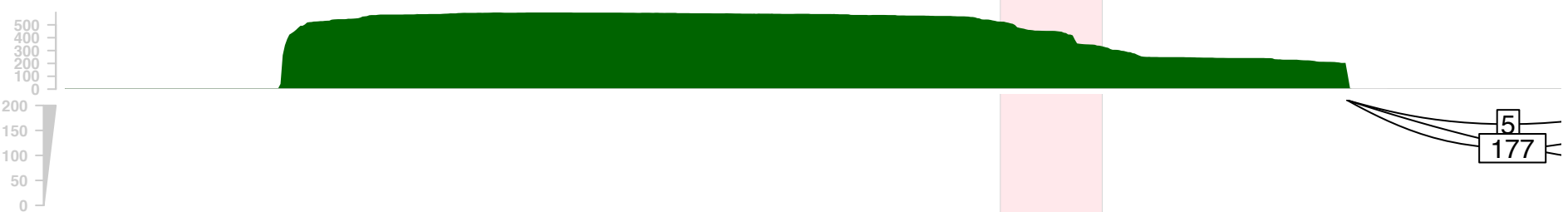
GENCODE v36
ENSG00000213977.8
ENSG00000213977.8
ENSG00000257950.3



cDNA

cDNA TX
annotation

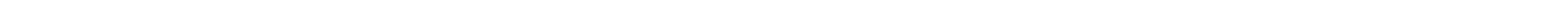
STR 38..167
STR 38..167
STR 38..167
STR 38..167



dRNA

dRNA TX
annotation

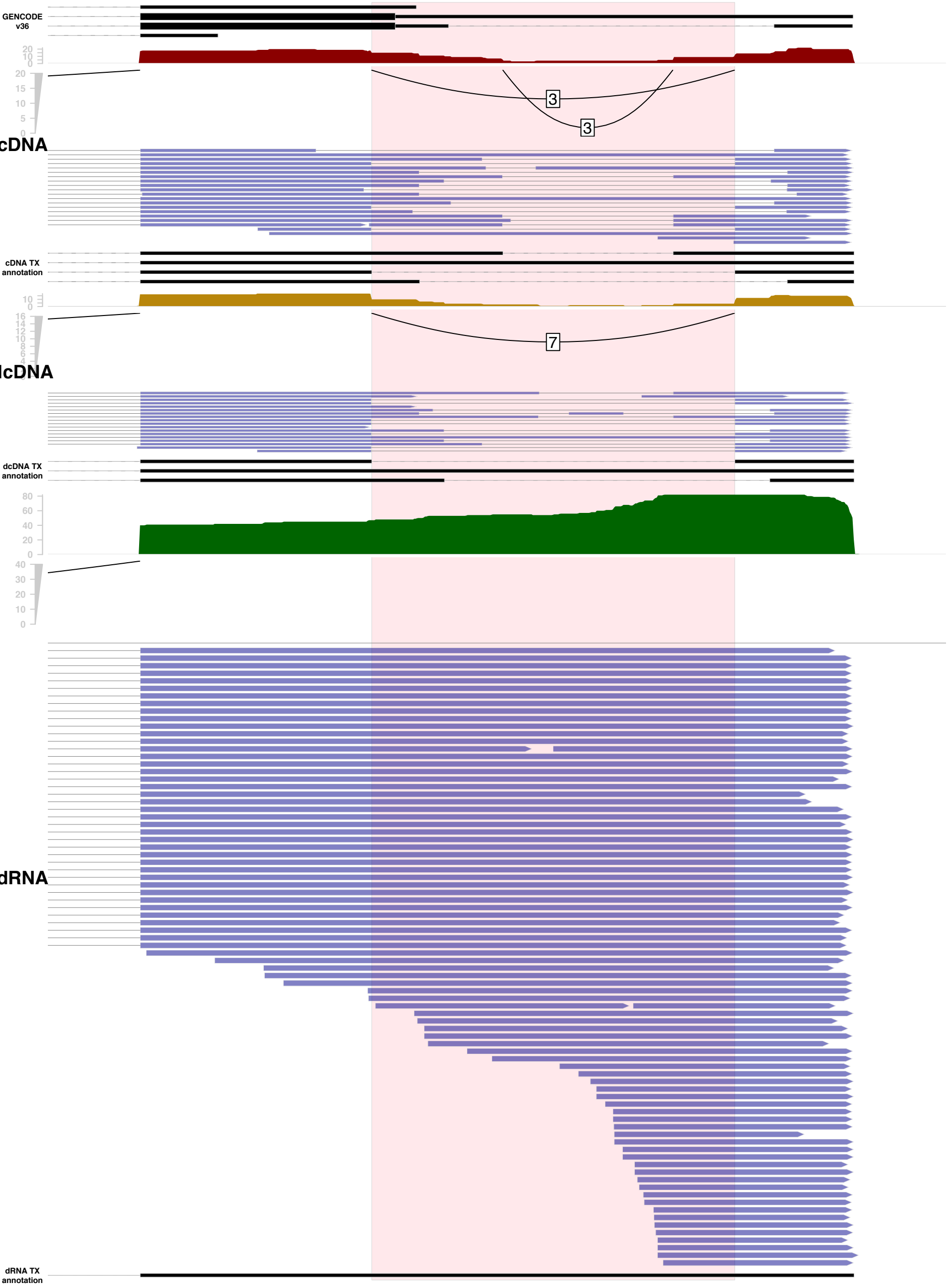
STR 98..11
STR 98..11
STR 98..11



chr1:28334920-28335708:+ MED18

Cell line: HepG2

Direct repeat sequence: CAGCTA



chr1:28334920-28335708:+ MED18

Cell line: K562

Direct repeat sequence: CAGCTA



chr1:28335161-28335708:+ MED18

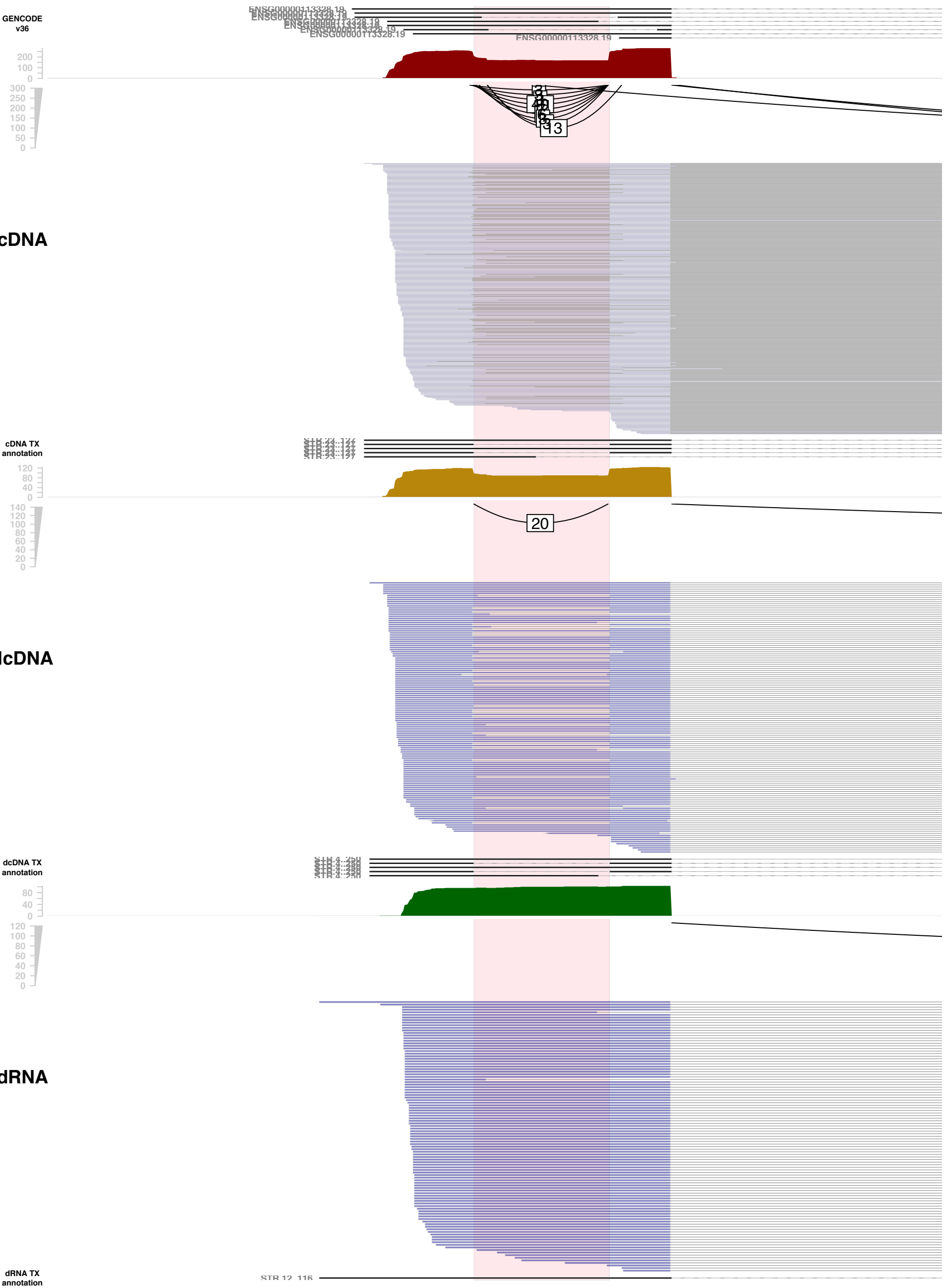
Cell line: K562

Direct repeat sequence: CAGC



chr5:163437659-163437758:+ CCNG1

Cell line: K562



chr6:170584411-170584491:- PDCD2

Cell line: K562



chr8:47976979-47977736:+ MCM4

Cell line: K562

GENCODE
v36

ENSG00000104738.18

100
50
0
70
60
50
40
30
20
10
0

12

cDNA

cDNA TX
annotation

60
40
20
0
60
50
40
30
20
10
0

8

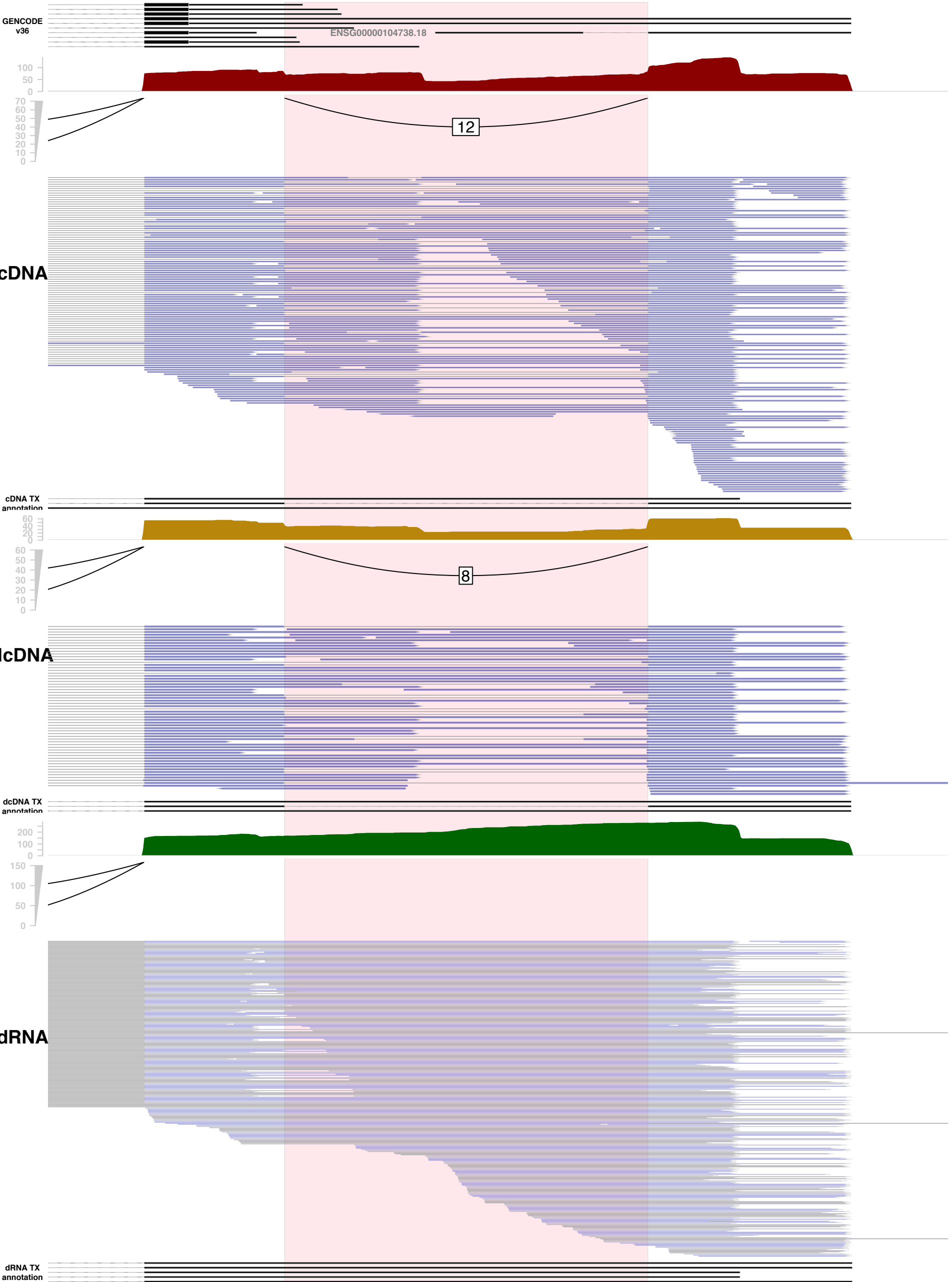
cDNA

dcDNA TX
annotation

200
100
0
150
100
50
0

dRNA

dRNA TX
annotation



chr9:127908169-127908317:- ST6GALNAC4

Cell line: K562

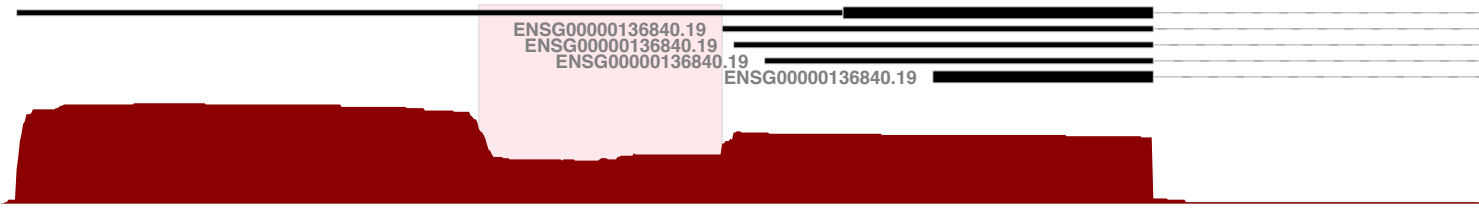
Direct repeat sequence: CTCCAC

GENCODE
v36

ENSG00000136840.19

ENSG00000136840.19
ENSG00000136840.19
ENSG00000136840.19

ENSG00000136840.19

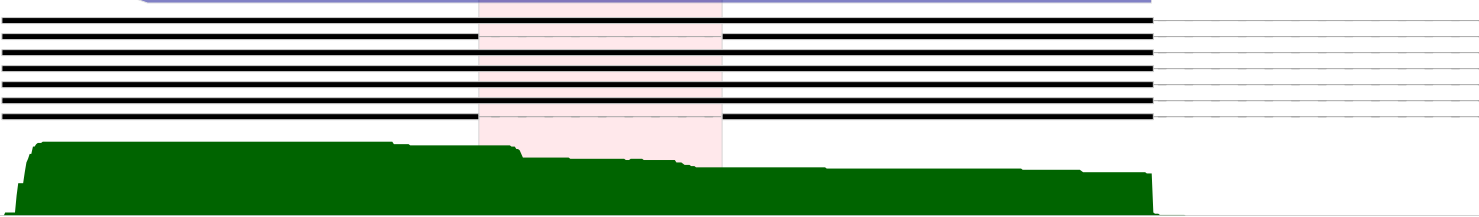


cDNA

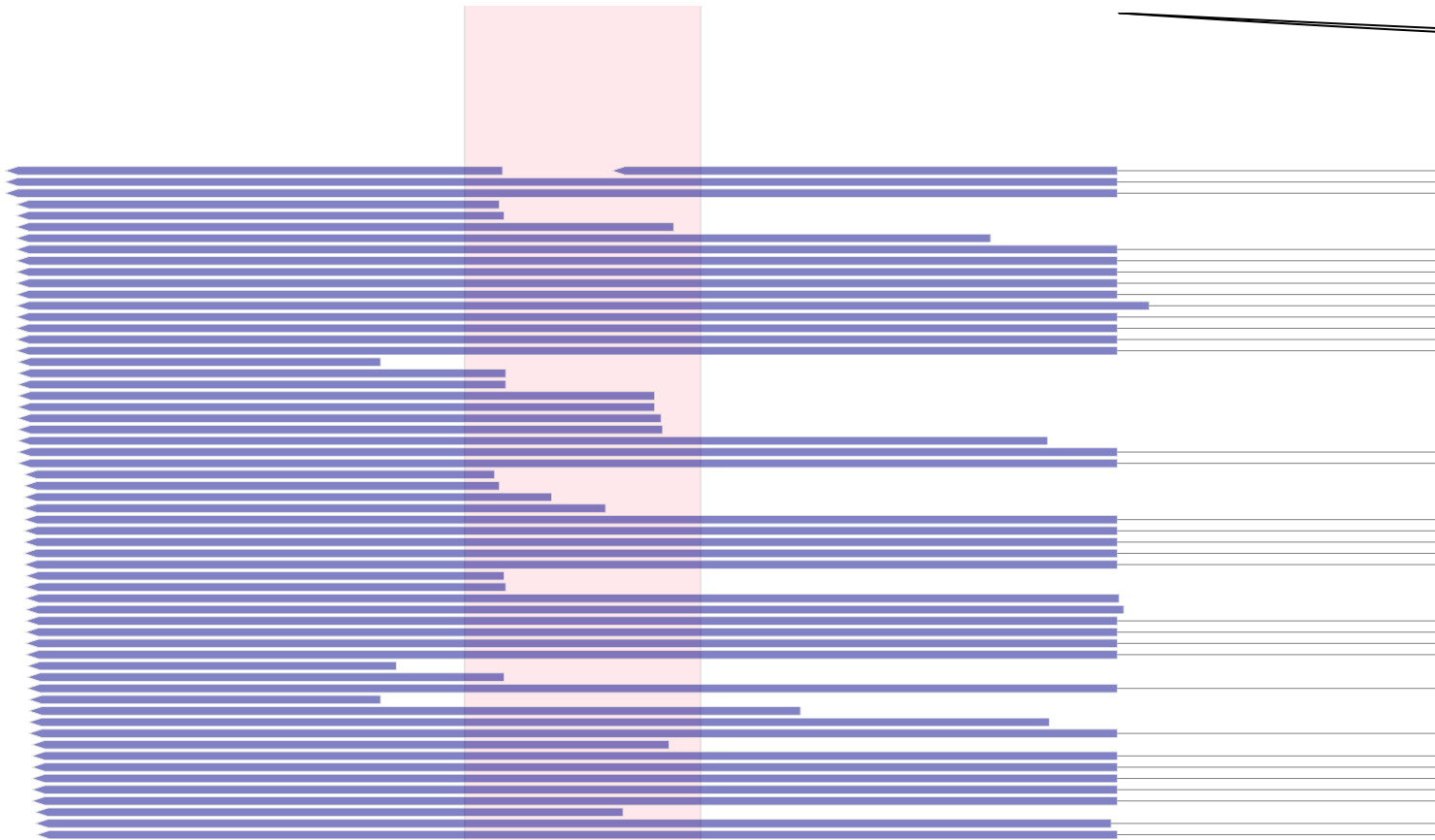


cDNA TX
annotation

STR.37..69
STR.37..69
STR.37..69
STR.37..69
STR.37..69
STR.37..69



dRNA

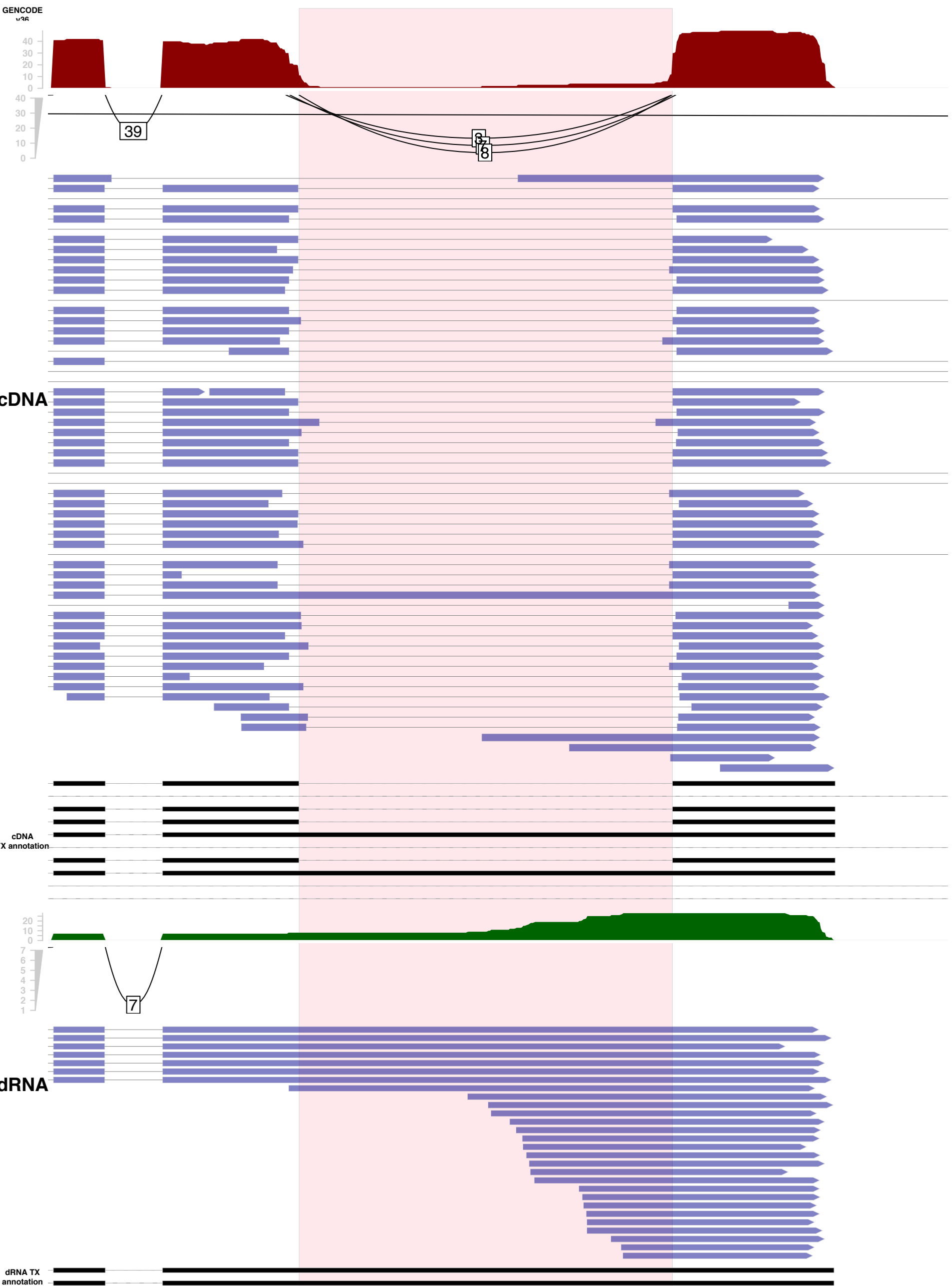


dRNA TX
annotation

STR.20..248
STR.20..248
STR.20..248
STR.20..248

chr11:6704862-6705515:+

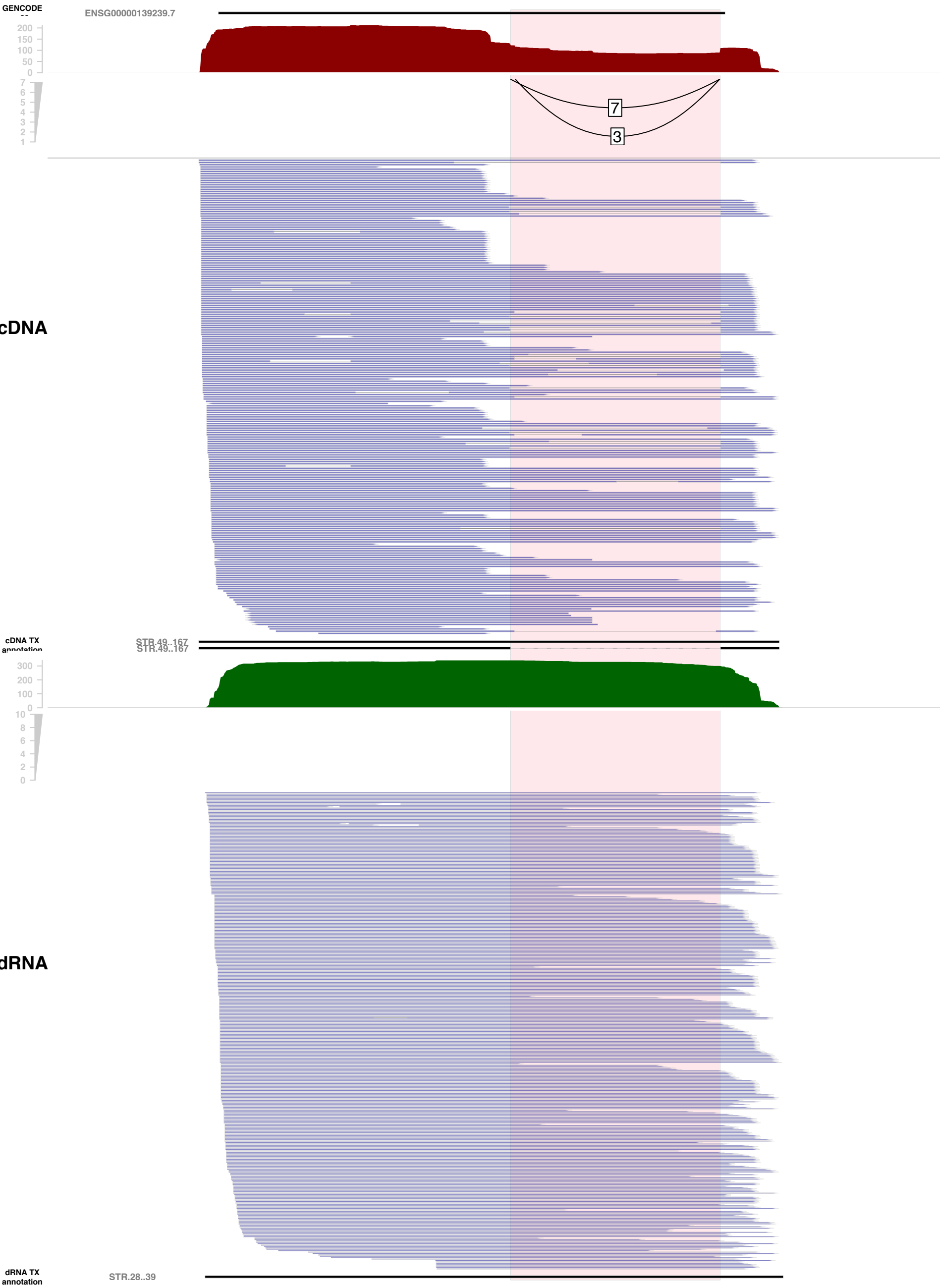
Cell line: K562



chr12:62965697-62965963:+ RPL14P1

Cell line: K562

Direct repeat sequence: CAAGAA



chr17:3663563-3663657:- TAX1BP3,P2RX5-TAX1BP3

Cell line: K562

Direct repeat sequence: GACCG

GENCODE v36
ENSG00000213977.8
ENSG00000213977.8
ENSG00000257950.3



cDNA

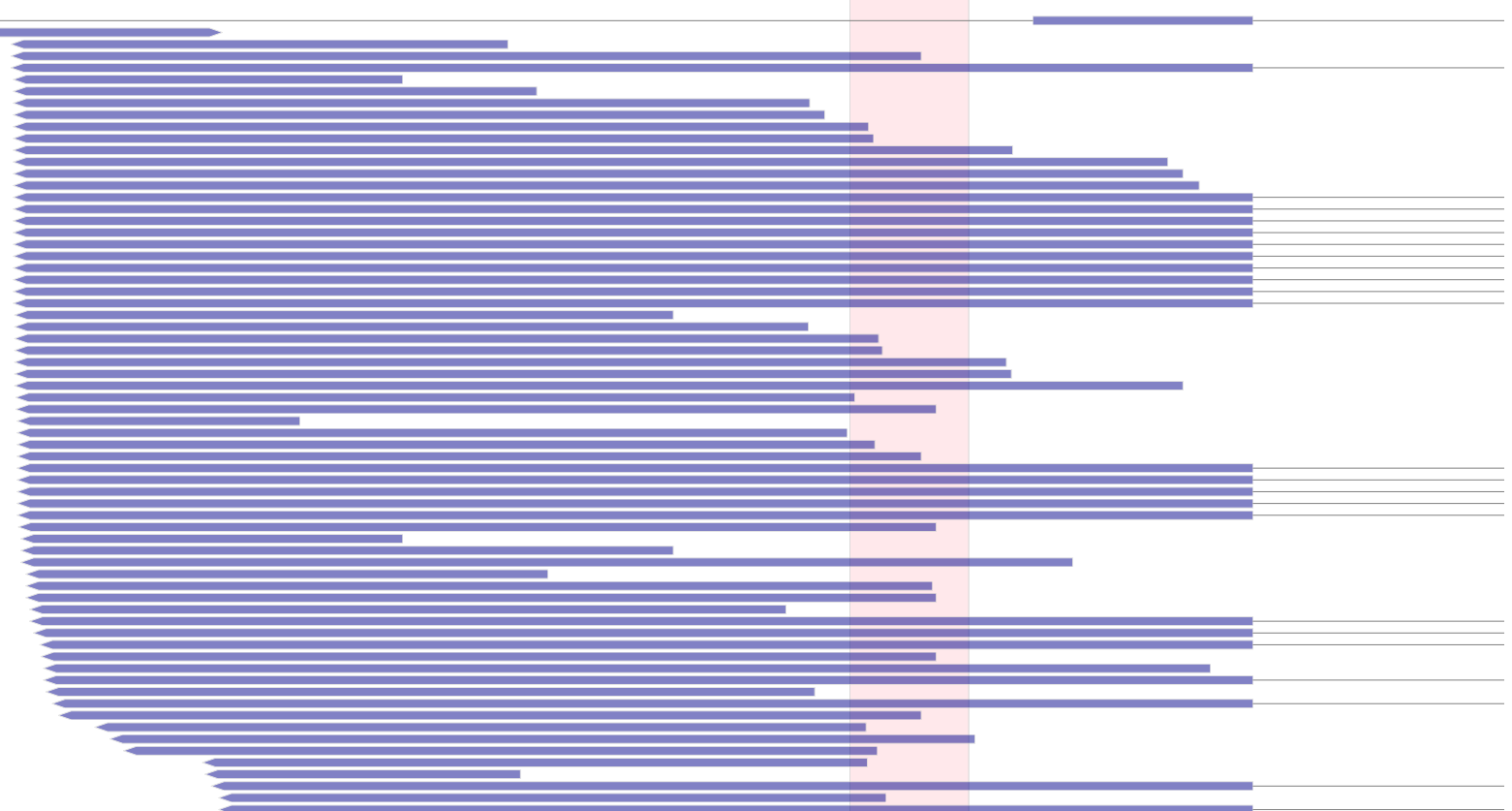


cDNA TX annotation

STR.59..472
STR.59..472
STR.59..472



dRNA



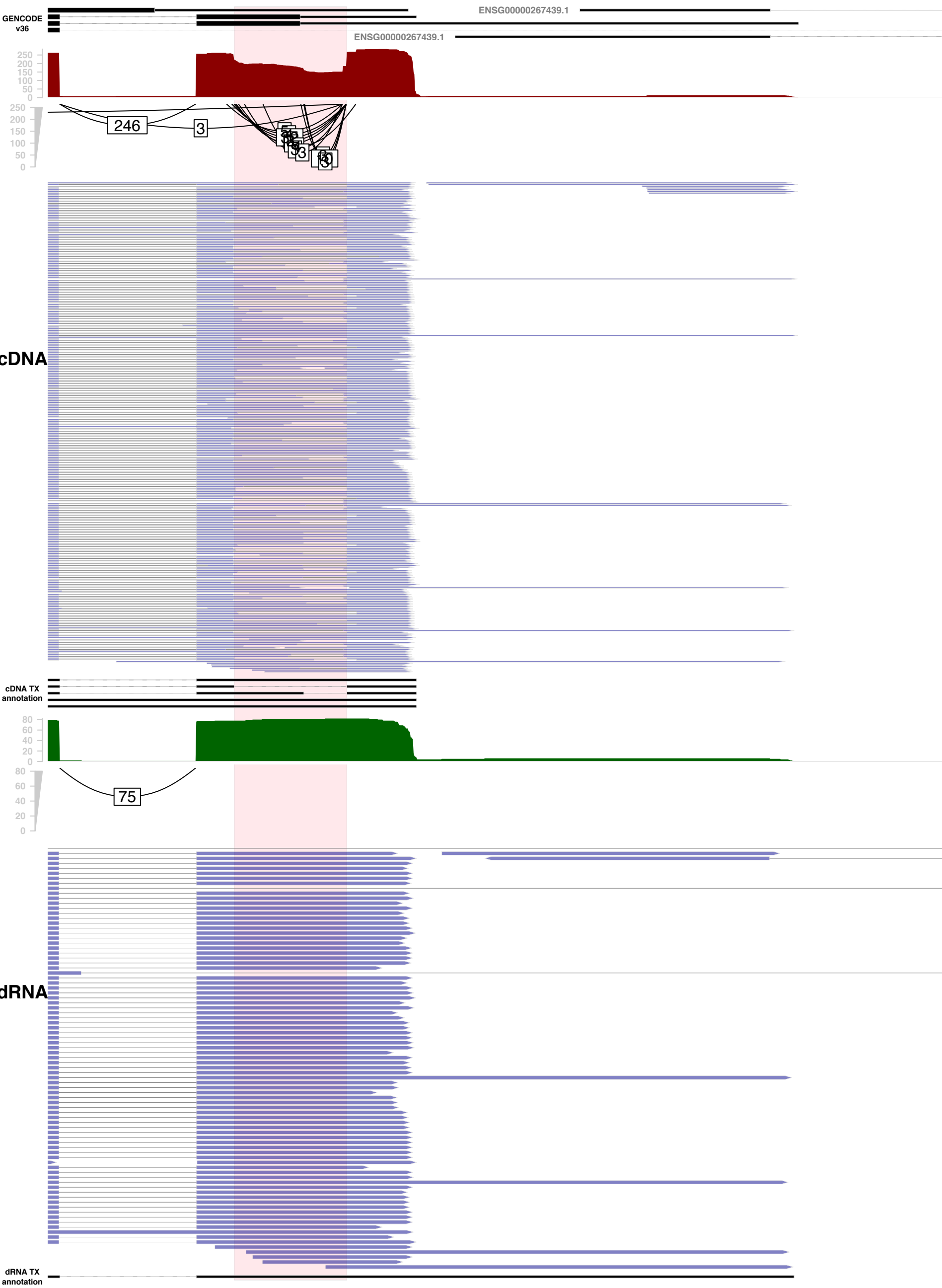
dRNA TX annotation

STR.34..193

chr19:35746759-35746910:+ PSENEN,AC002398.9

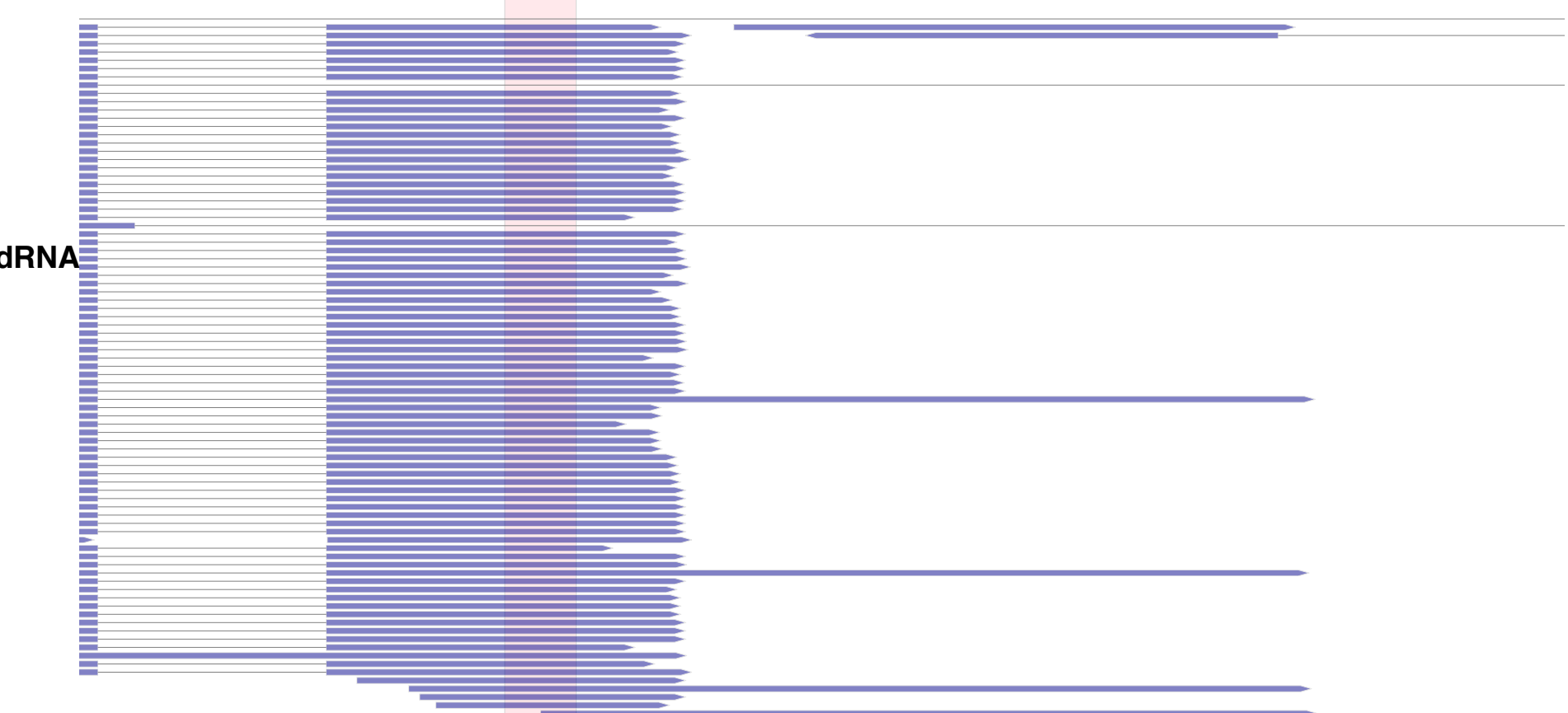
Cell line: K562

Direct repeat sequence: CCTG



chr19:35746853-35746910:+ PSENEN,AC002398.9

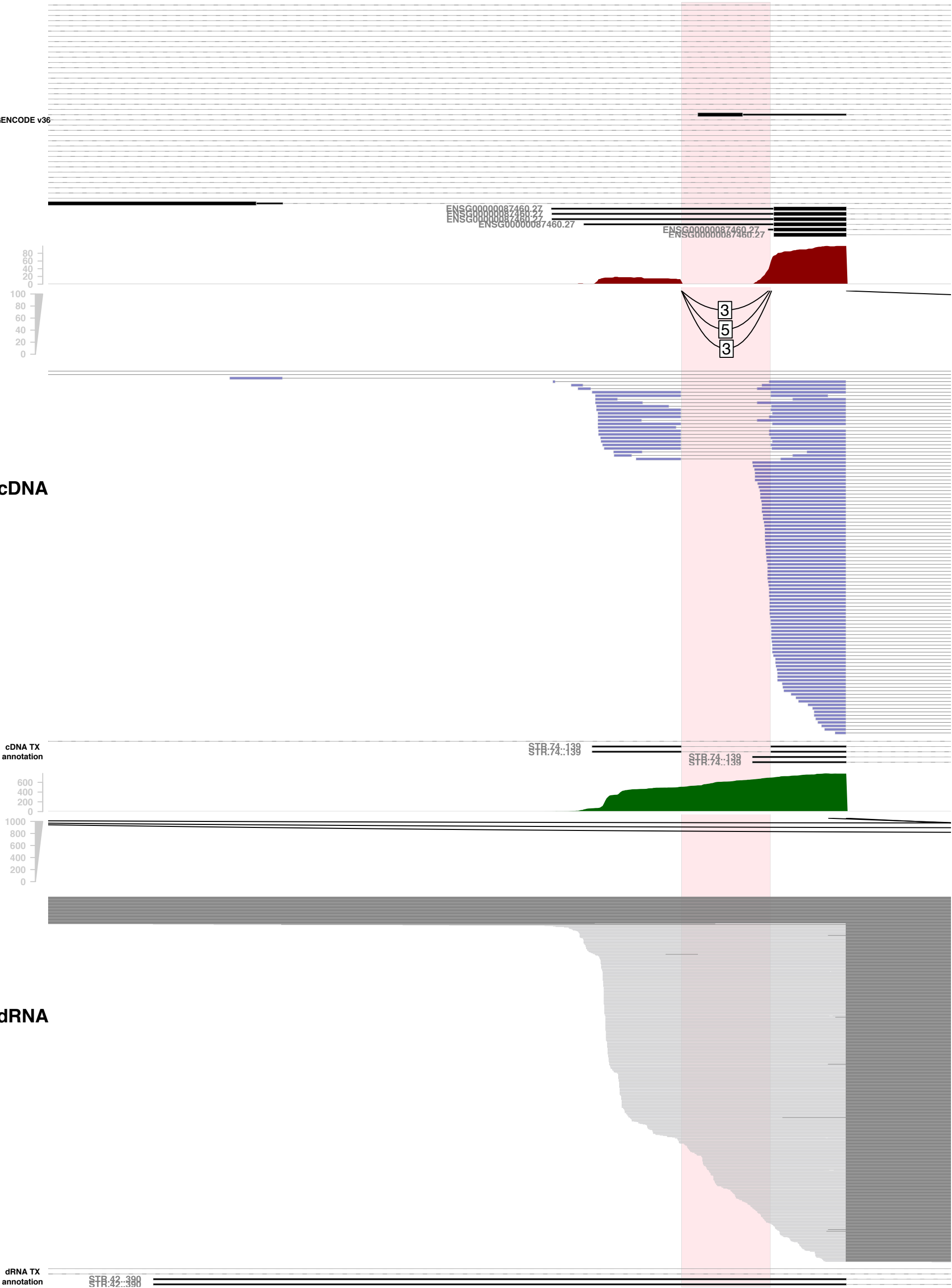
Cell line: K562



chr20:58891551-58891720:+ GNAS

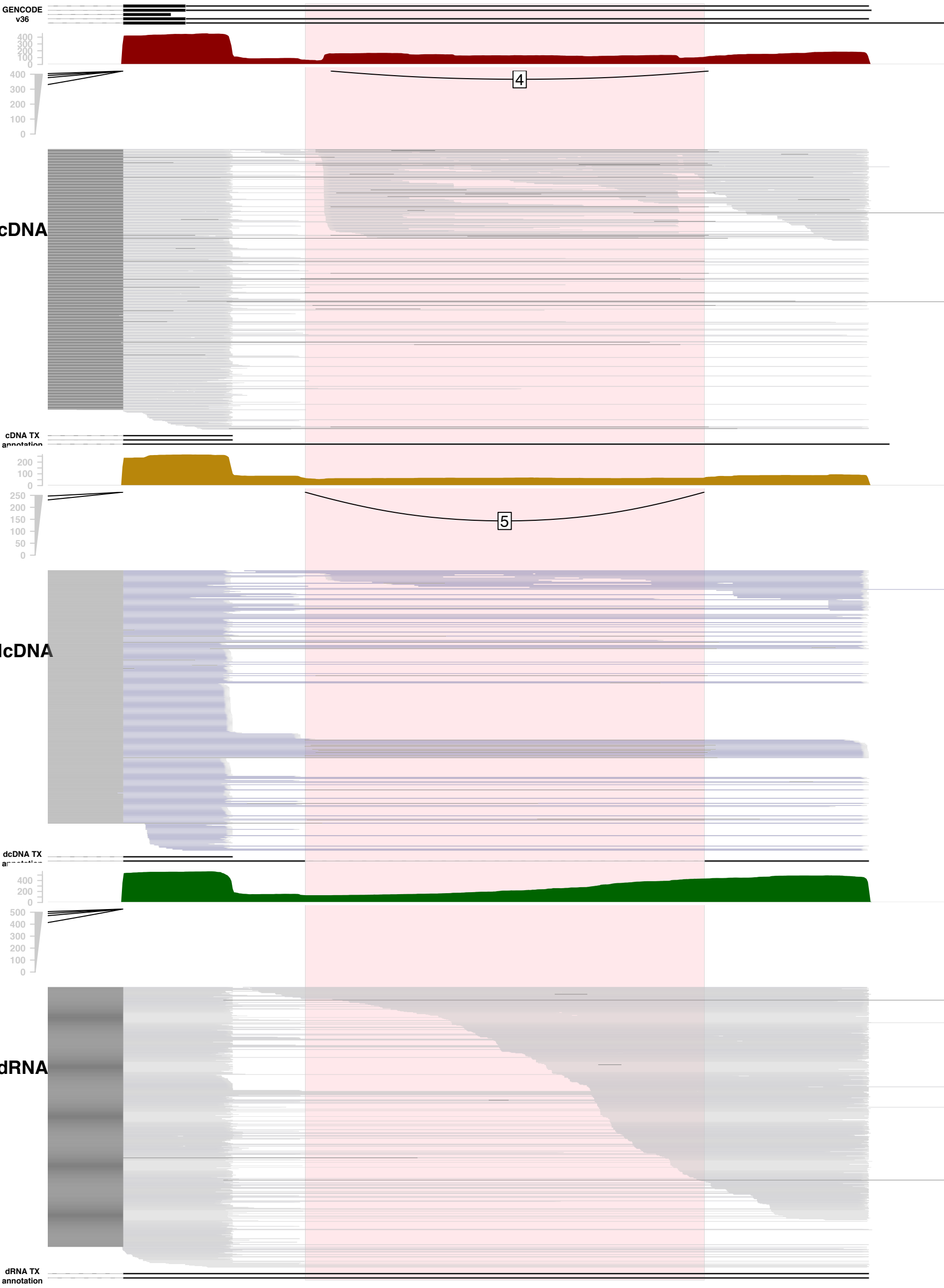
Cell line: K562

Direct repeat sequence: CCGCC



chr4:56459858-56460922:+ PAICS

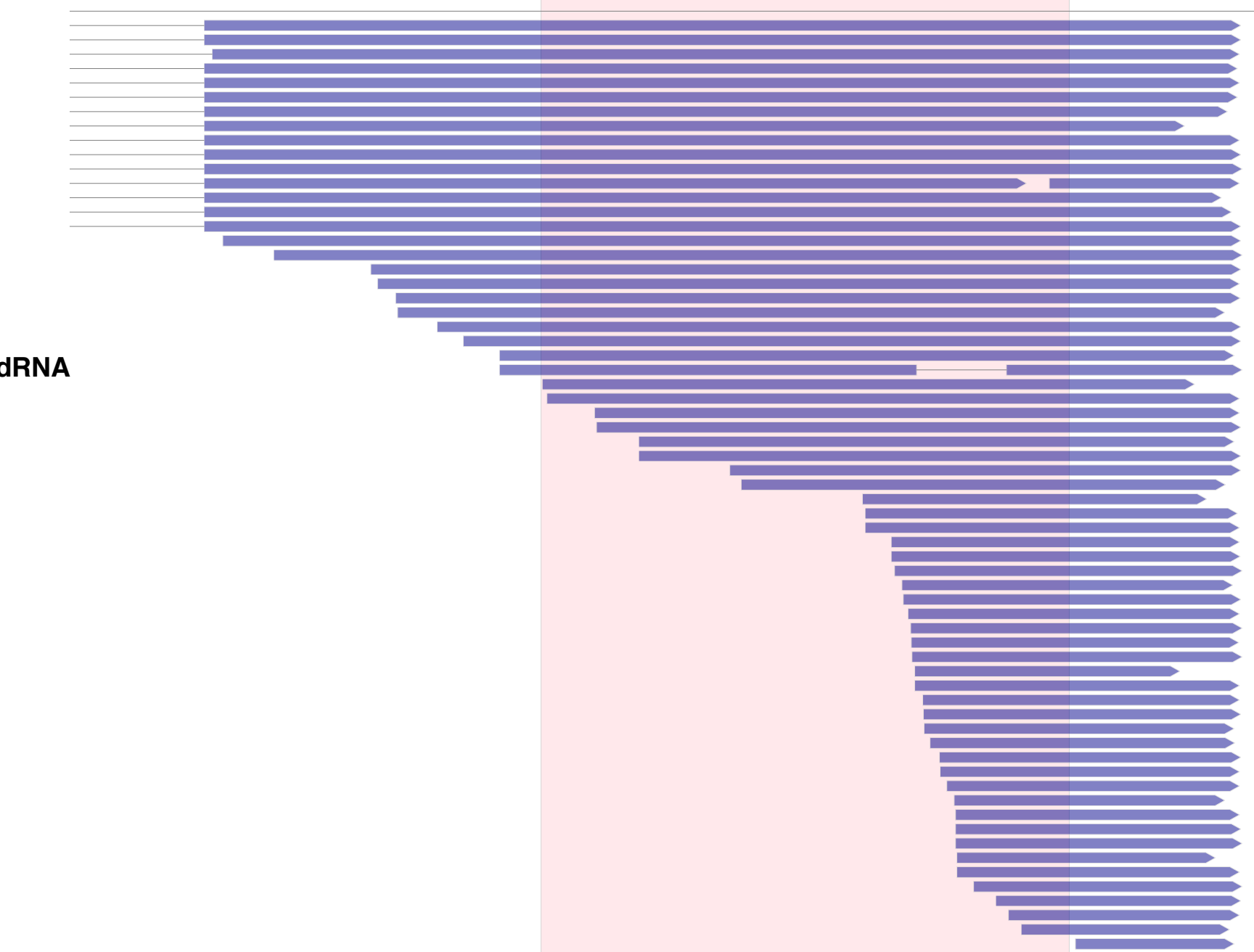
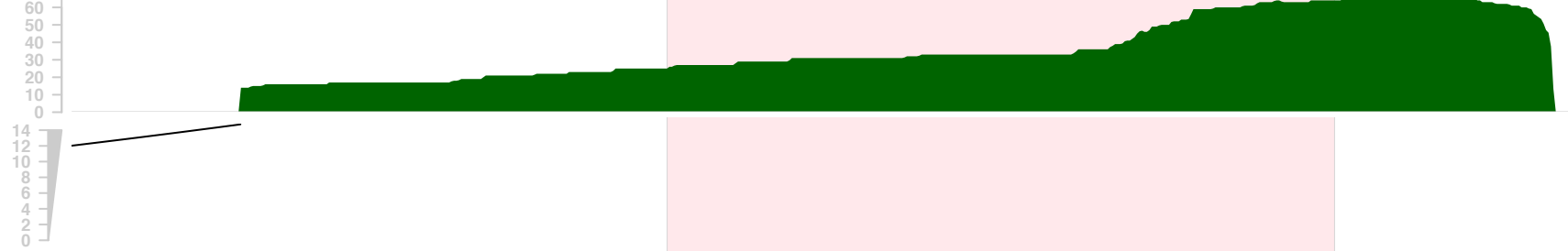
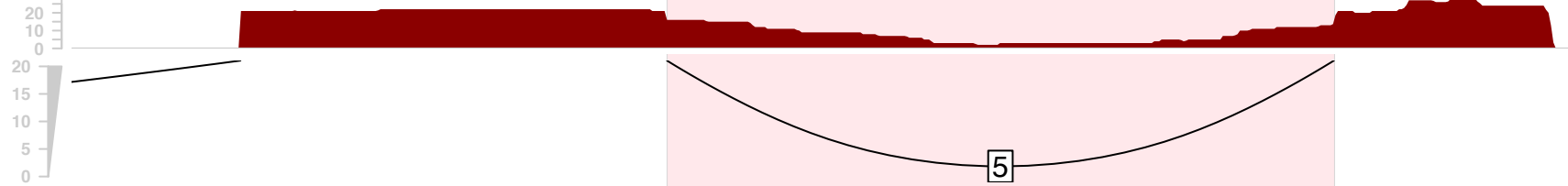
Cell line: K562



chr1:28334920-28335708:+ MED18

Cell line: MCF7

Direct repeat sequence: CAGCTA



chr17:3663563-3663657:- TAX1BP3,P2RX5-TAX1BP3

Cell line: MCF7

Direct repeat sequence: GACCG

GENCODE v36
ENSG00000213977.8
ENSG00000213977.8
ENSG00000257950.3



cDNA TX annotation
STR.32..975
STR.32..975

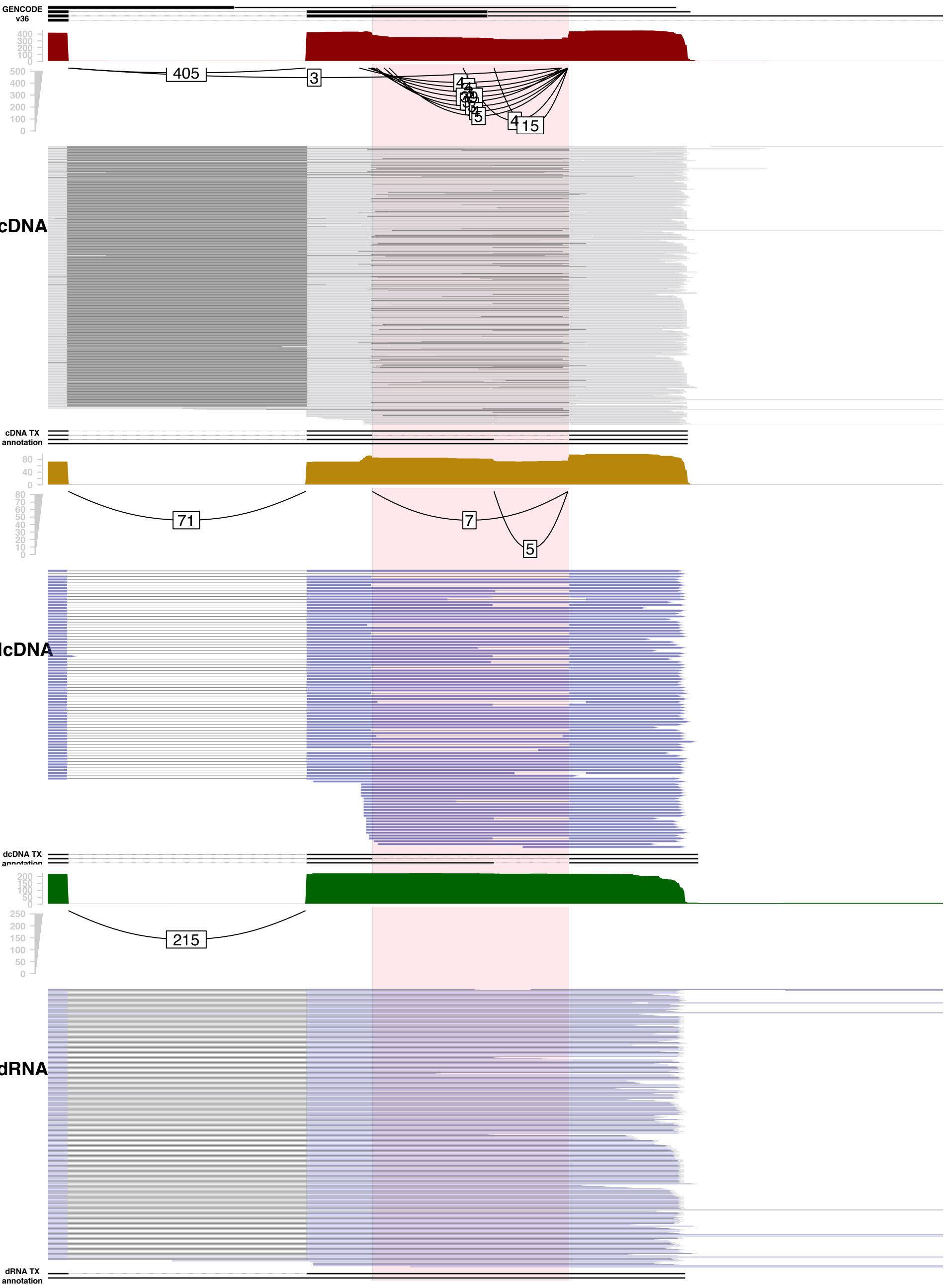


dRNA TX annotation
STR.56..132

chr19:35746759-35746910:+ PSENEN,AC002398.9

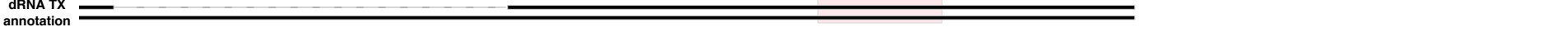
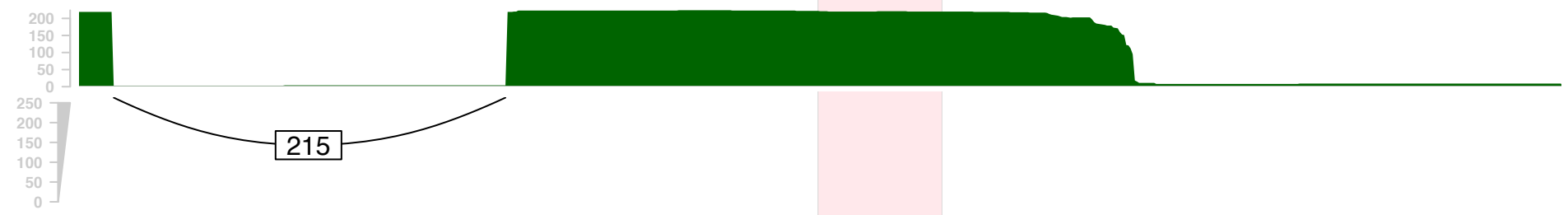
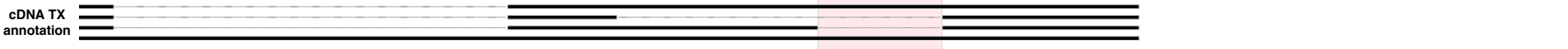
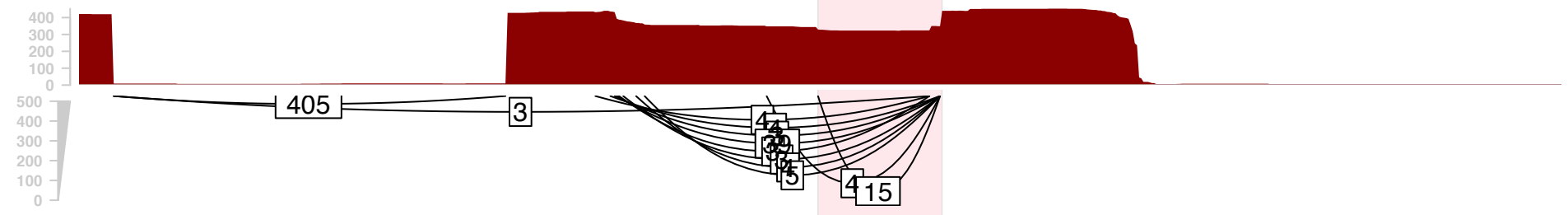
Cell line: MCF7

Direct repeat sequence: CCTG



chr19:35746853-35746910:+ PSENEN,AC002398.9

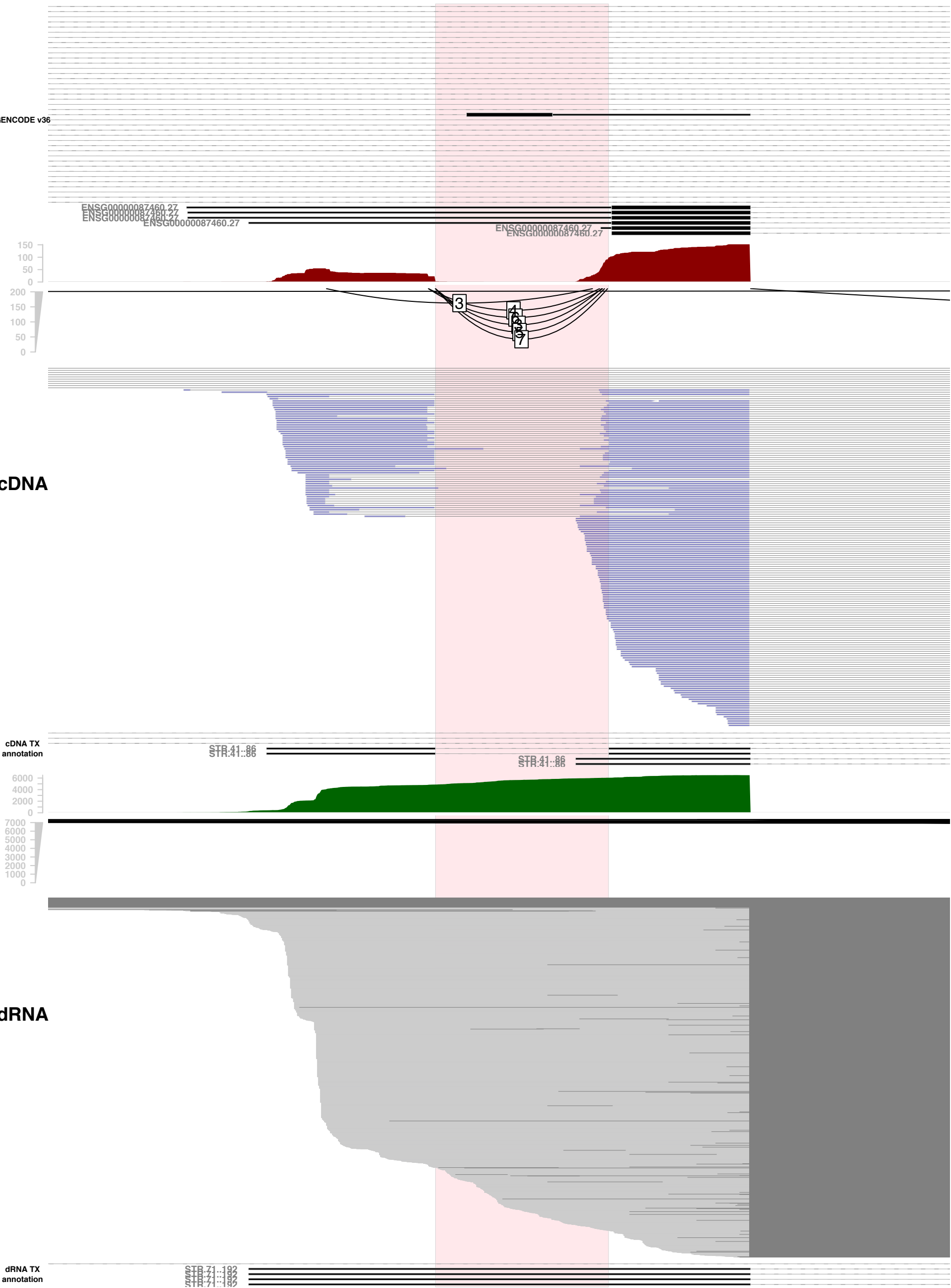
Cell line: MCF7



chr20:58891551-58891723:+ GNAS

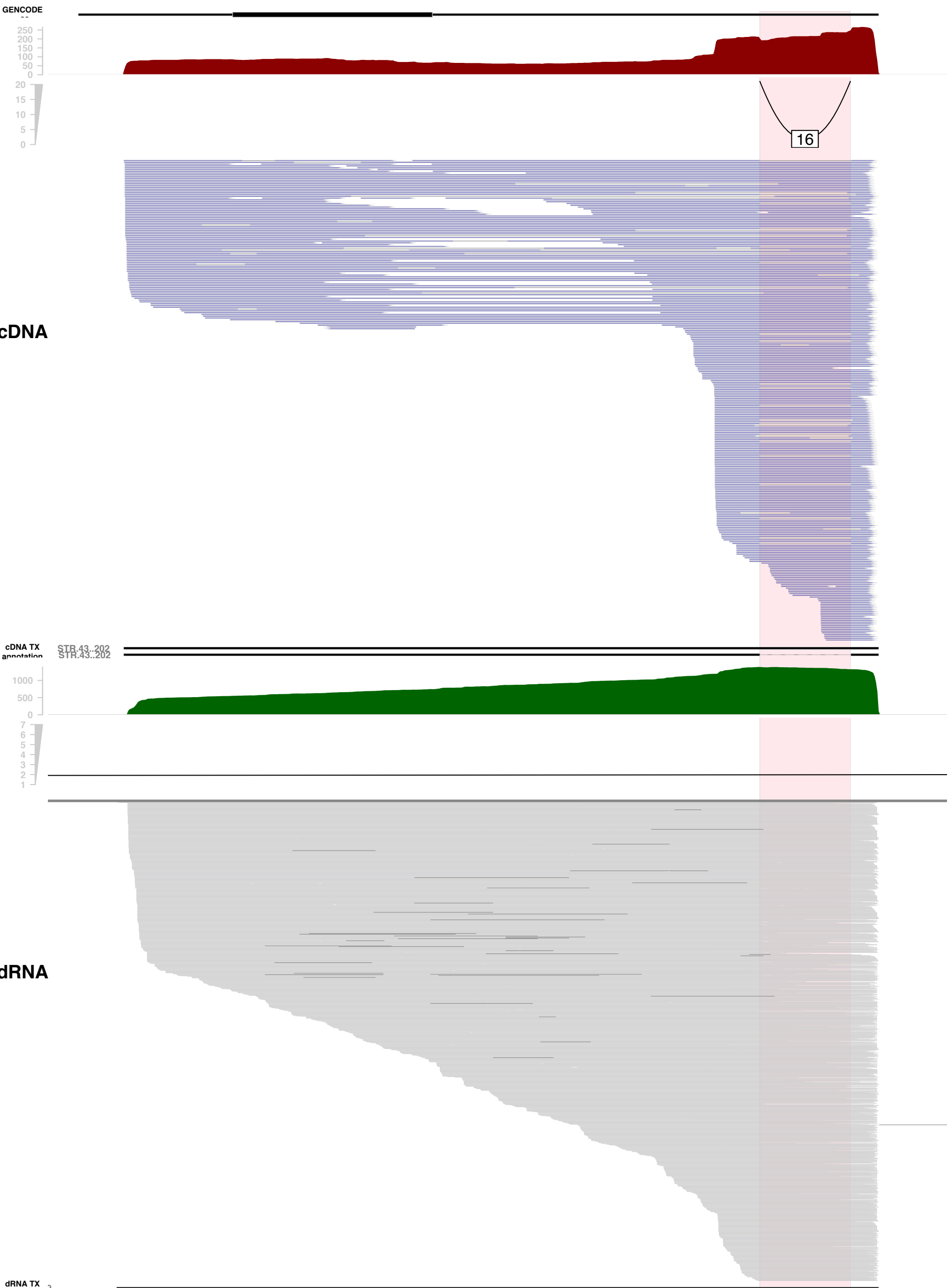
Cell line: MCF7

Direct repeat sequence: CCGCC



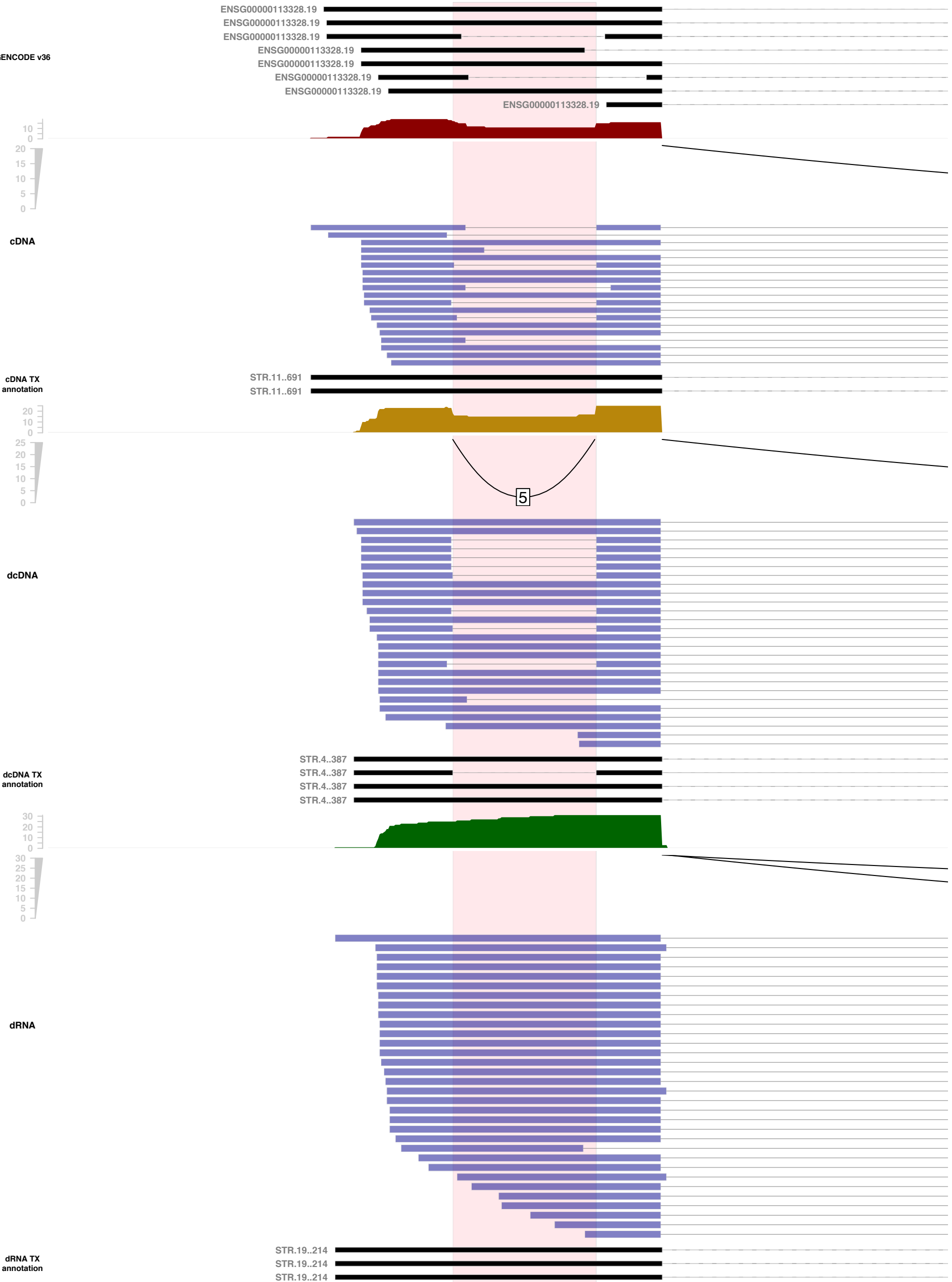
chr22:37807089-37807354:+ H1FO

Cell line: MCF7



chr5:163437659-163437758:+ CCNG1

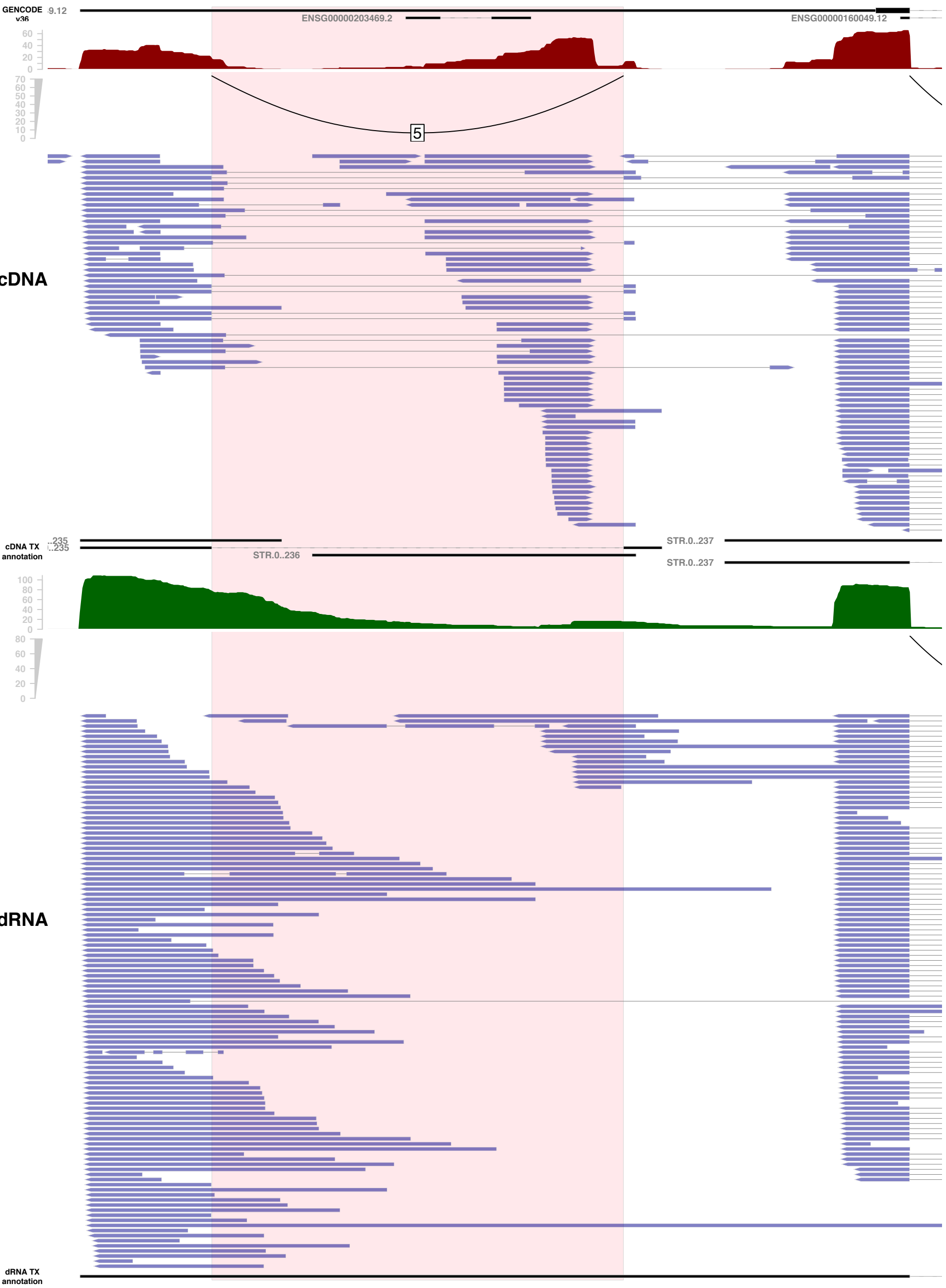
Cell line: MCF7



chr1:10457345-10459914:- DFFA

Cell line: NA12878

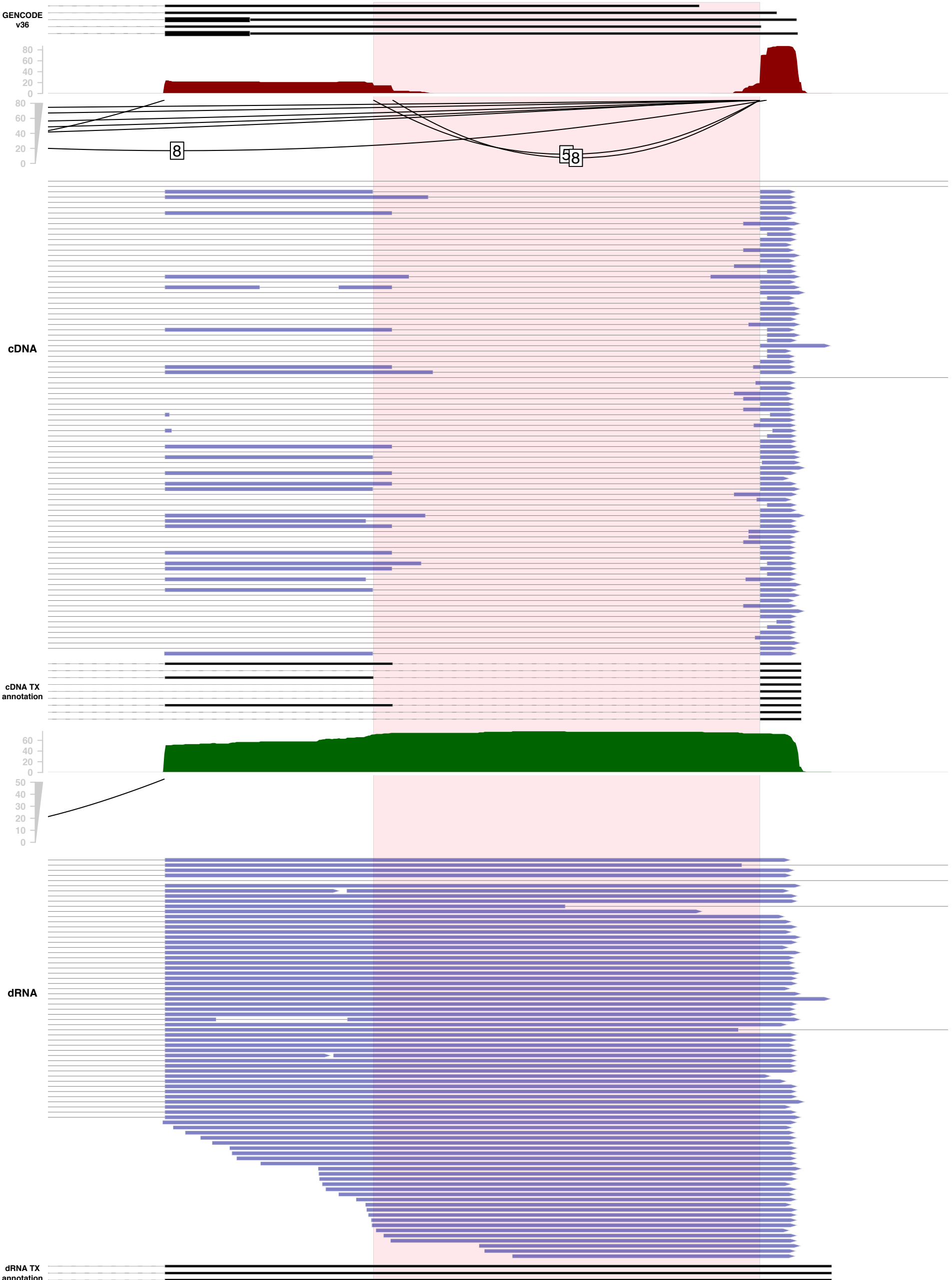
Direct repeat sequence: AACATAGCAAGACCC



chr19:45703262-45703924:+ QPCTL

Cell line: NA12878

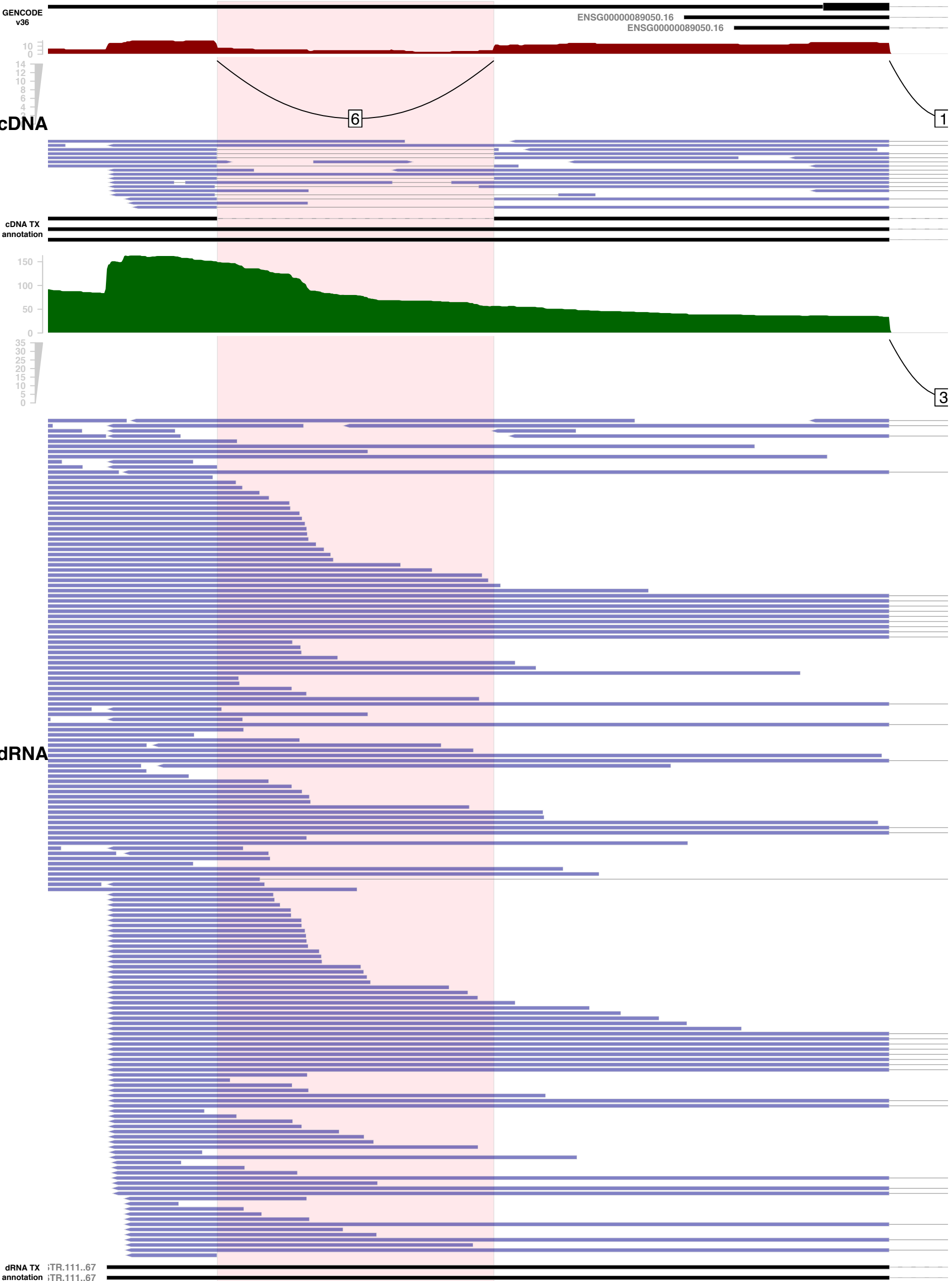
Direct repeat sequence: CAGCC



chr20:18487692-18488637:- RBBP9

Cell line: NA12878

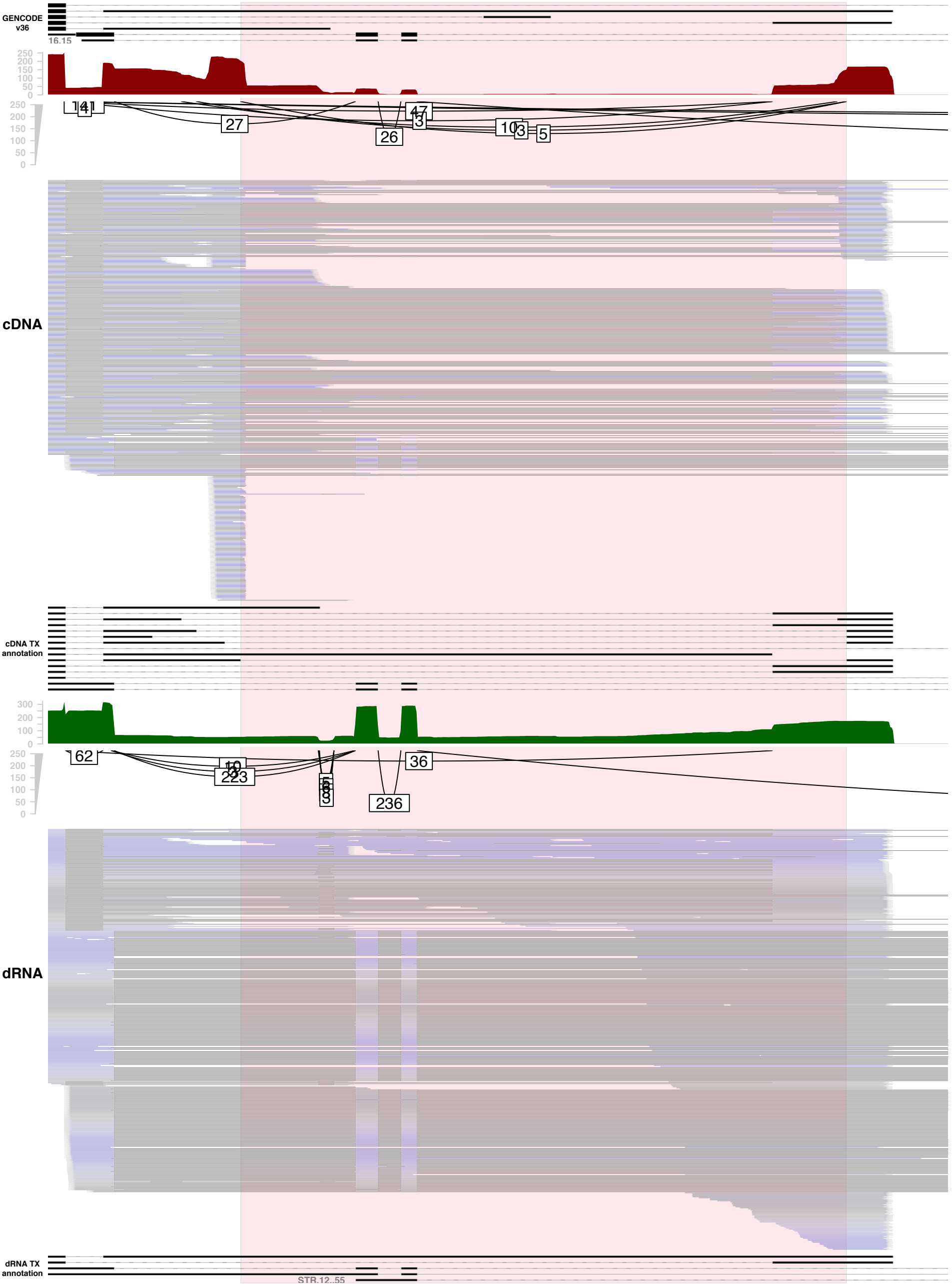
Direct repeat sequence: CATG



chr2:37202365-37204573:+ CEBPZOS

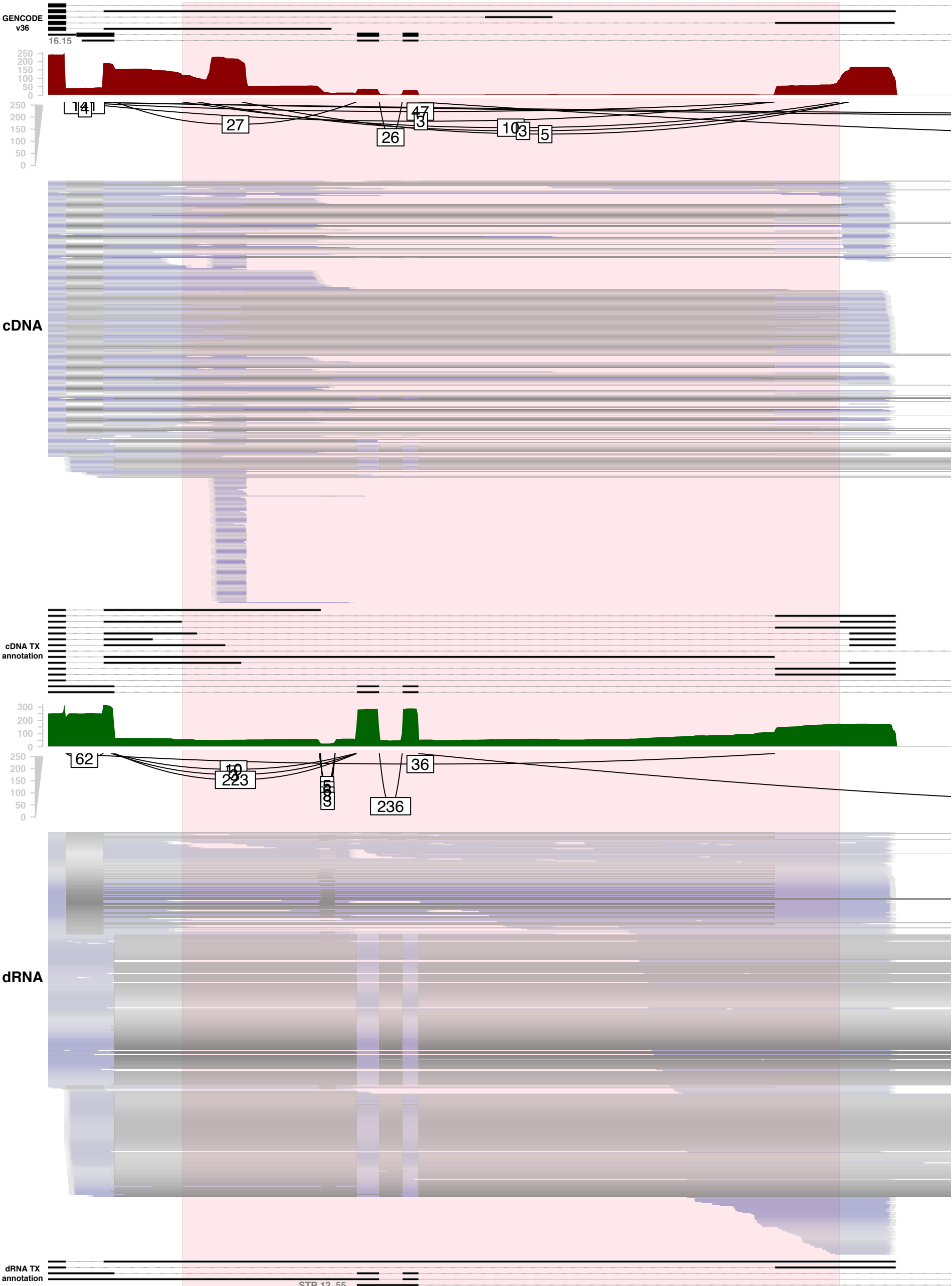
Cell line: NA12878

Direct repeat sequence: CAGCCA



chr2:37202149-37204539:+ CEBPZOS

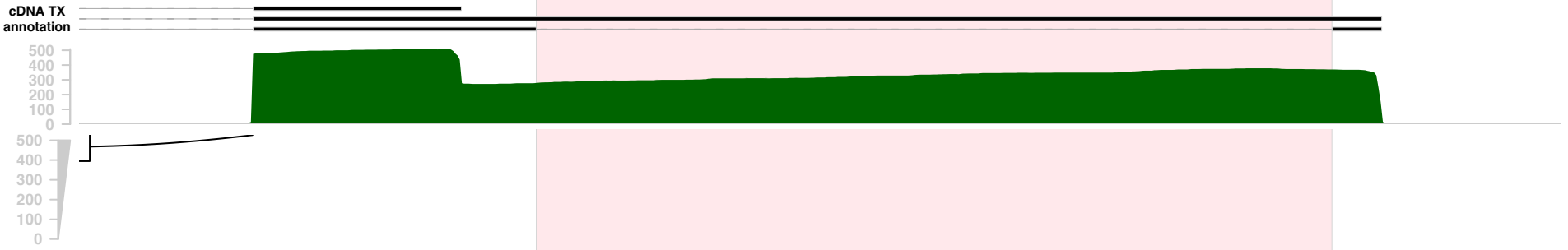
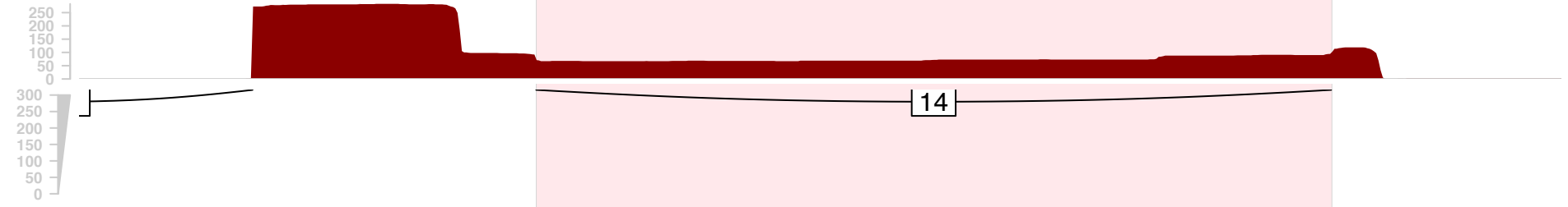
Cell line: NA12878



chrX:119583452-119584366:+ UBE2A

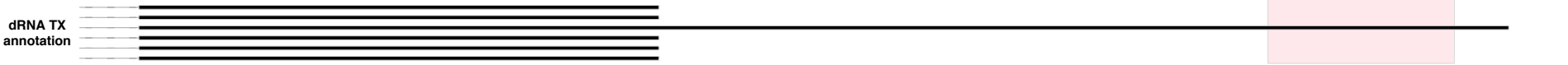
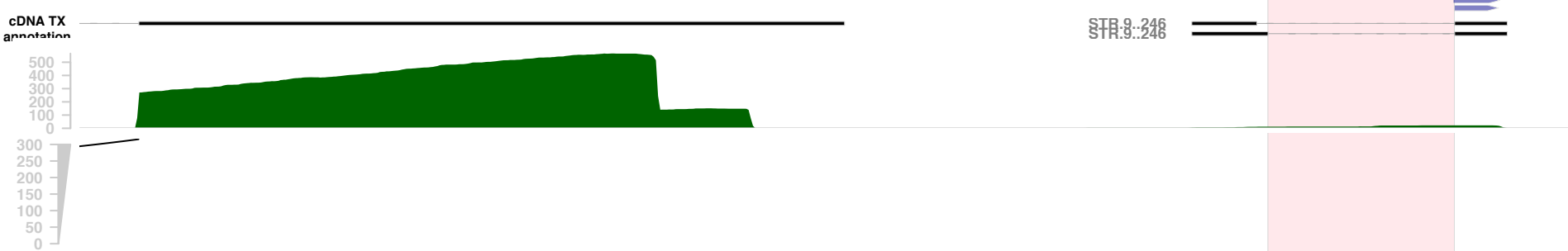
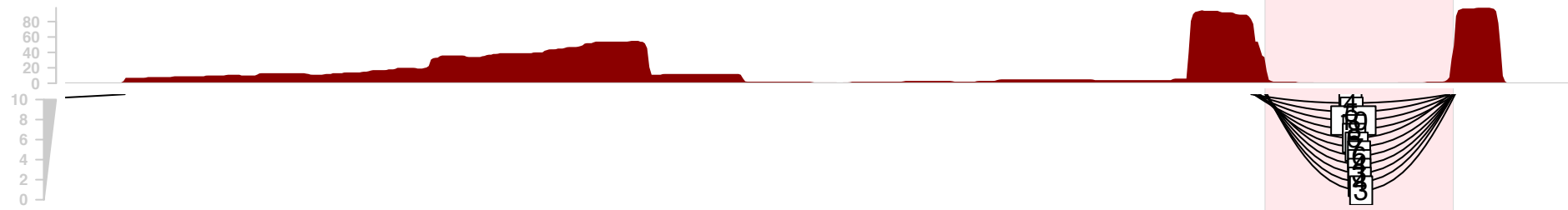
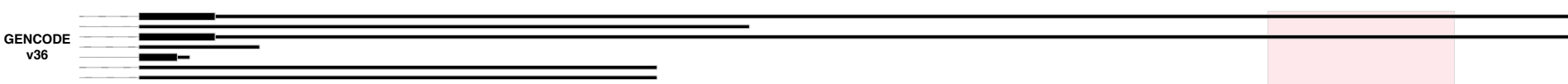
Cell line: NA12878

Direct repeat sequence: ATGTA



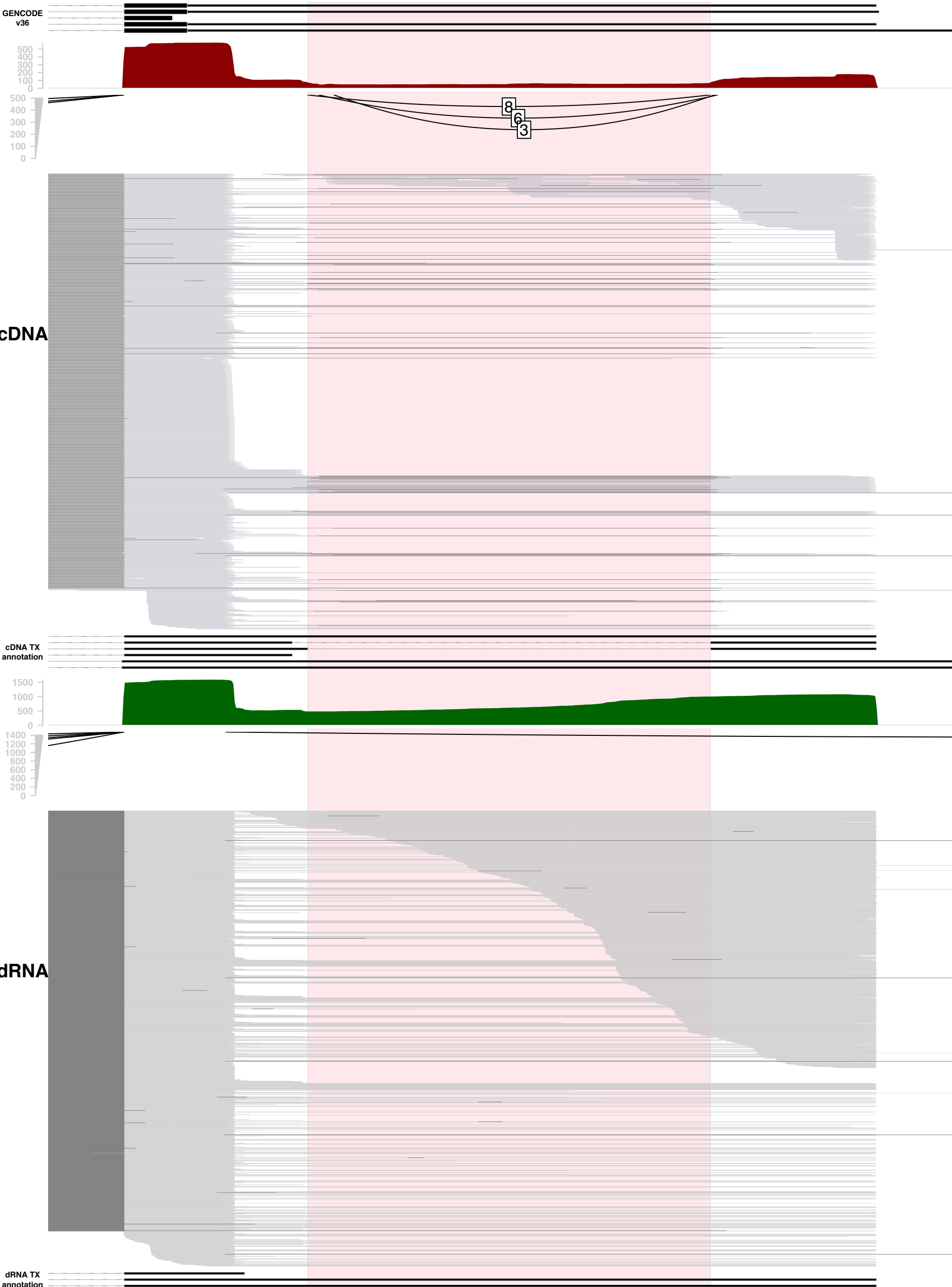
chr2:113204982-113205613:+ PSD4

Cell line: NA12878



chr4:56459858-56460922:+ PAICS

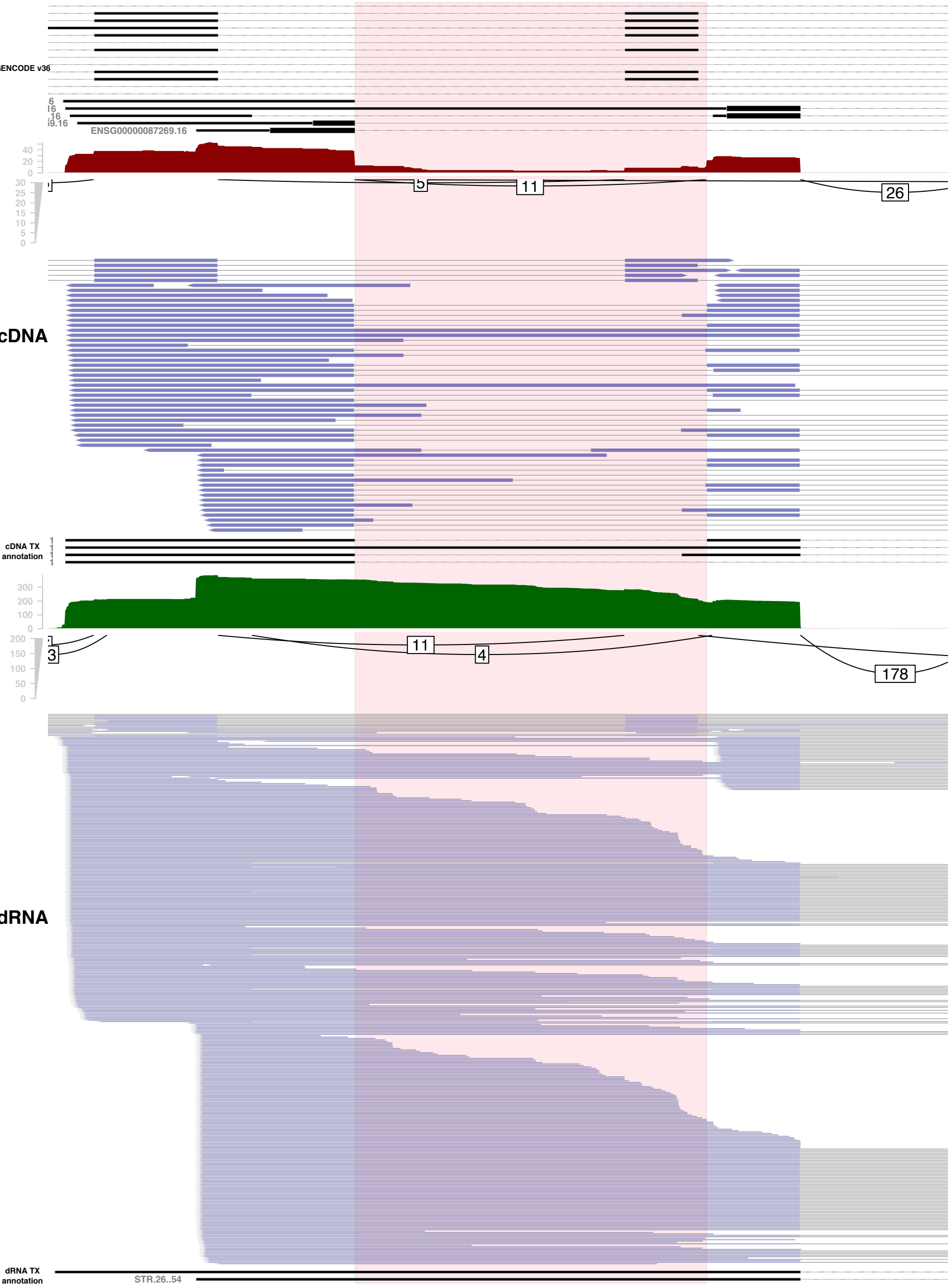
Cell line: NA12878



chr4:2938328-2938803:- NOP14

Cell line: NA12878

Direct repeat sequence: CTGG



chr5:163437659-163437758:+ CCNG1

Cell line: NA12878

GENCODE v36

ENSG00000113328.19
ENSG00000113328.19
ENSG00000113328.19
ENSG00000113328.19
ENSG00000113328.19
ENSG00000113328.19
ENSG00000113328.19

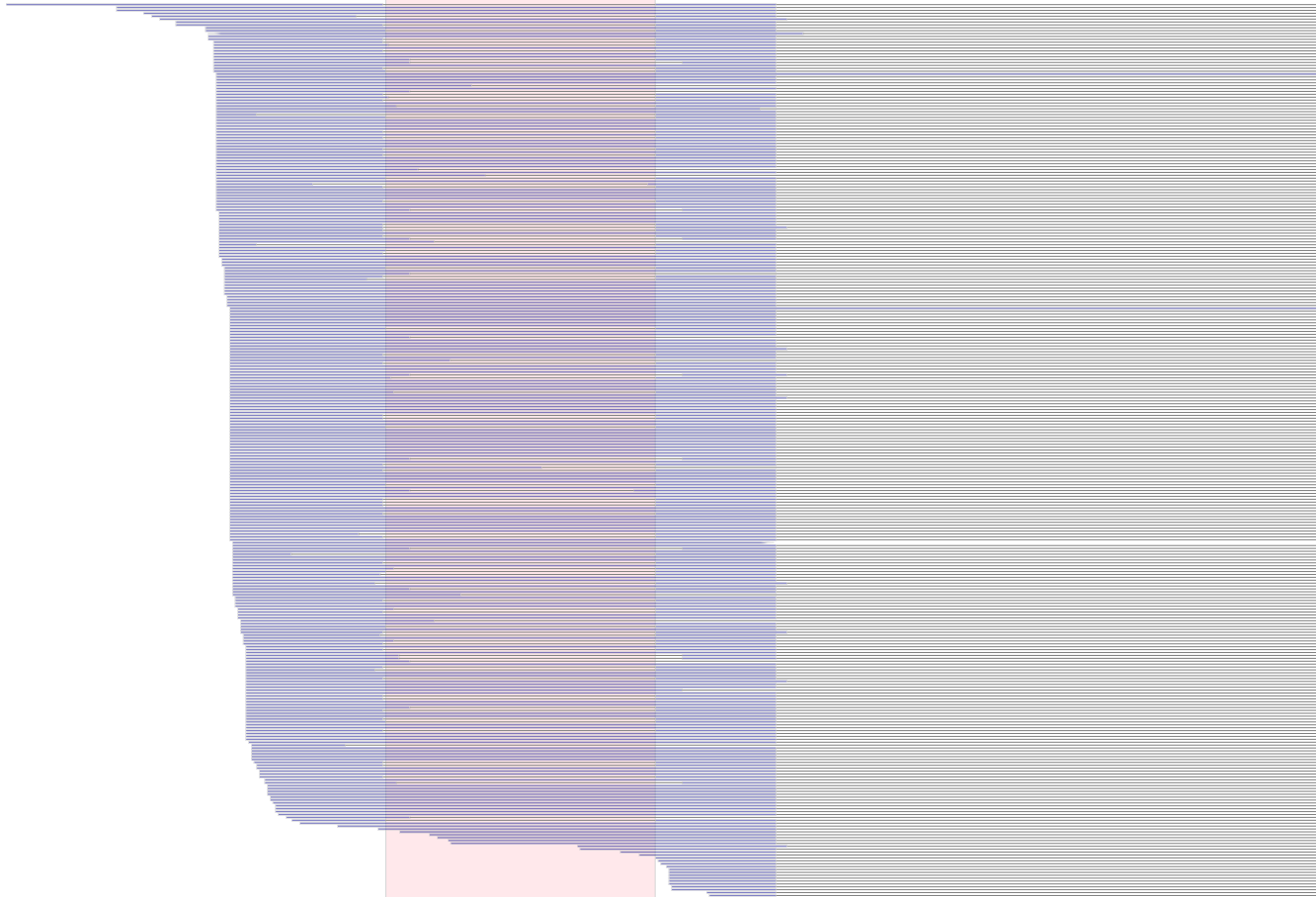
250
200
150
100
50
0



300
250
200
150
100
50
0



cDNA



cDNA TX annotation

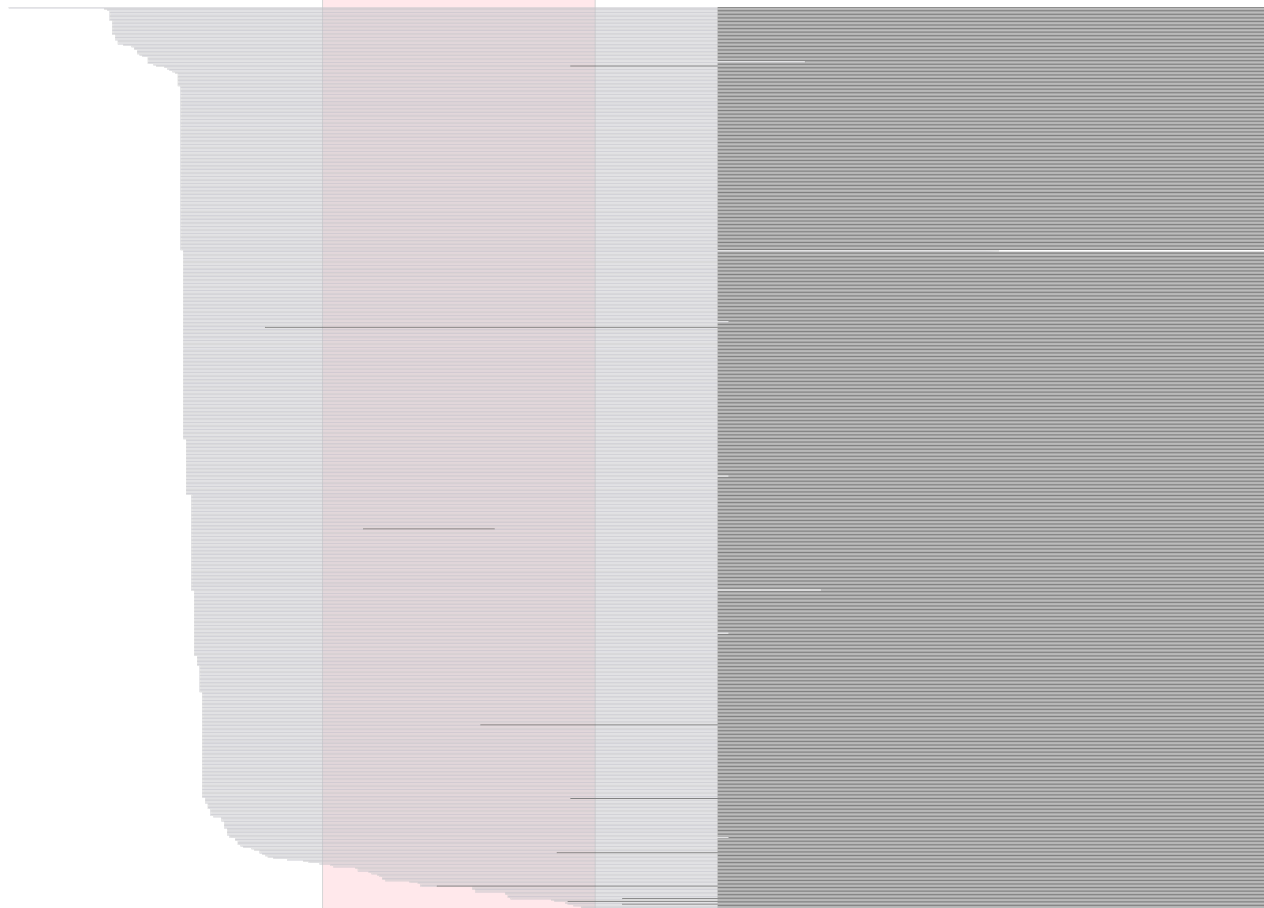
STR.21..142
STR.21..142
STR.21..142
STR.21..142

600
500
400
300
200
100
0



700
600
500
400
300
200
100
0

dRNA



dRNA TX annotation

STR.33..83

chr5:180835052-180835421:+ LINC00847

Cell line: NA12878

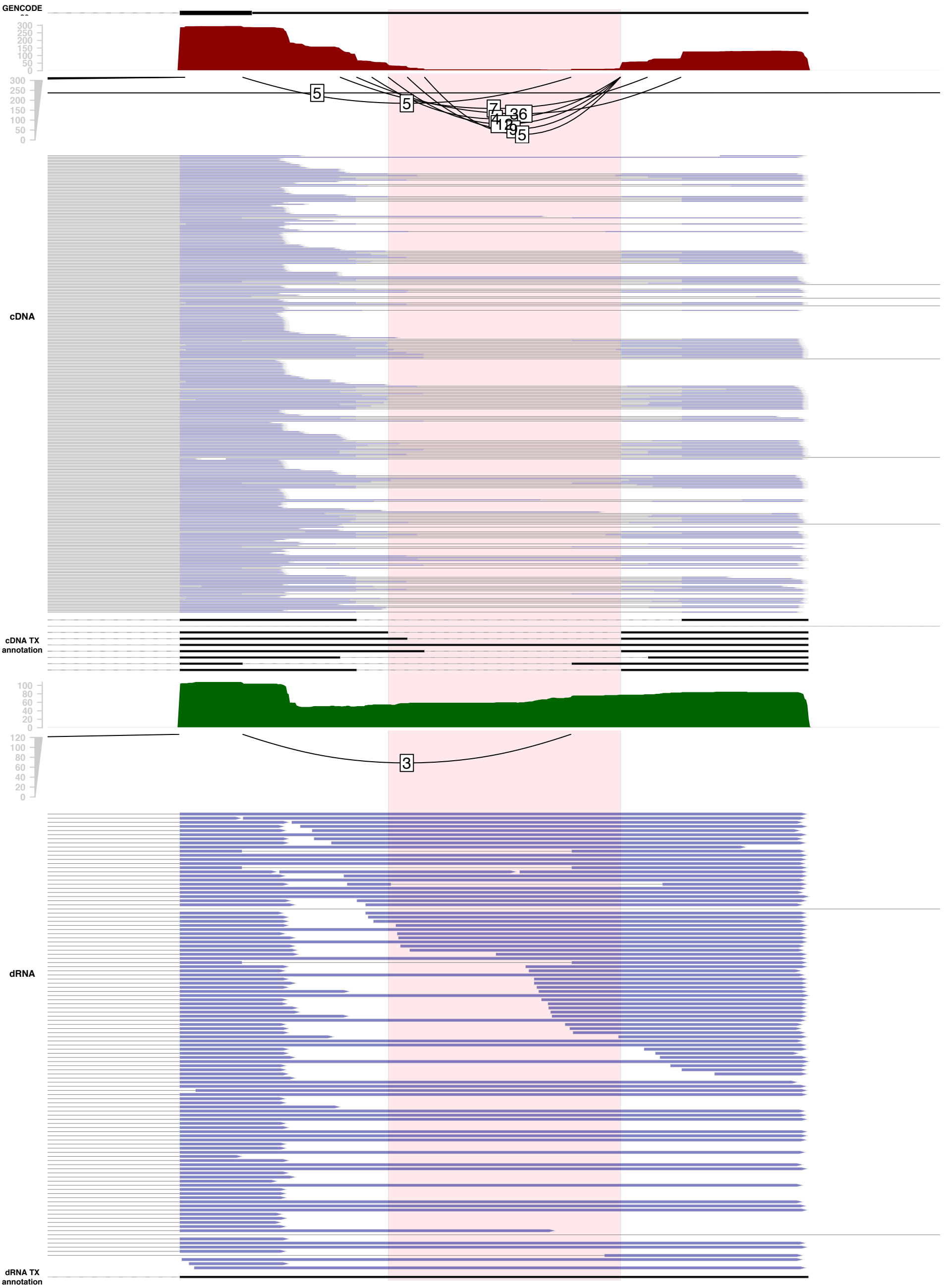
Direct repeat sequence: GCCTTC



chr6:70588932-70589284:+ SDHAF4

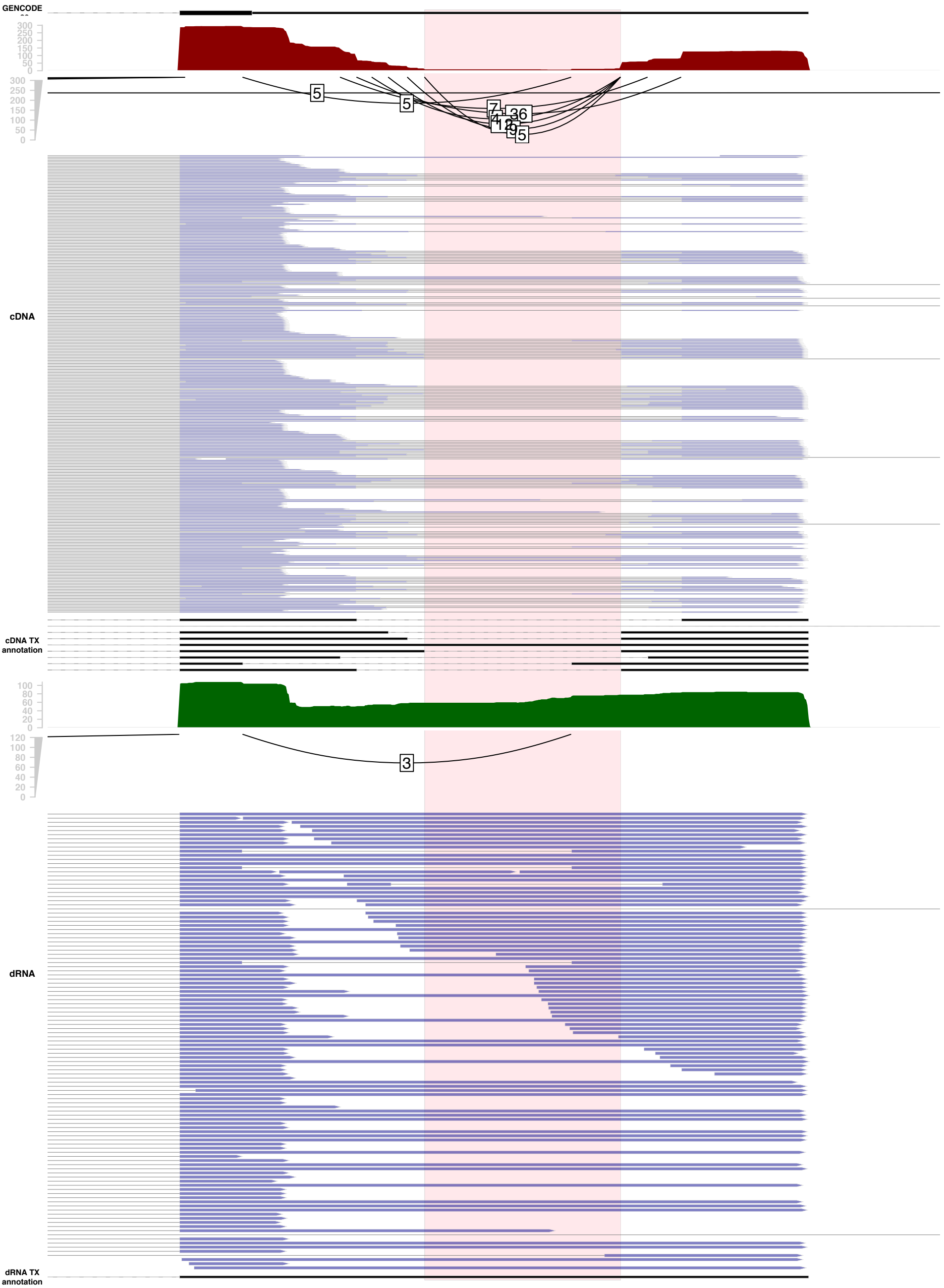
Cell line: NA12878

Direct repeat sequence: GCCT



chr6:70588987-70589284:+ SDHAF4

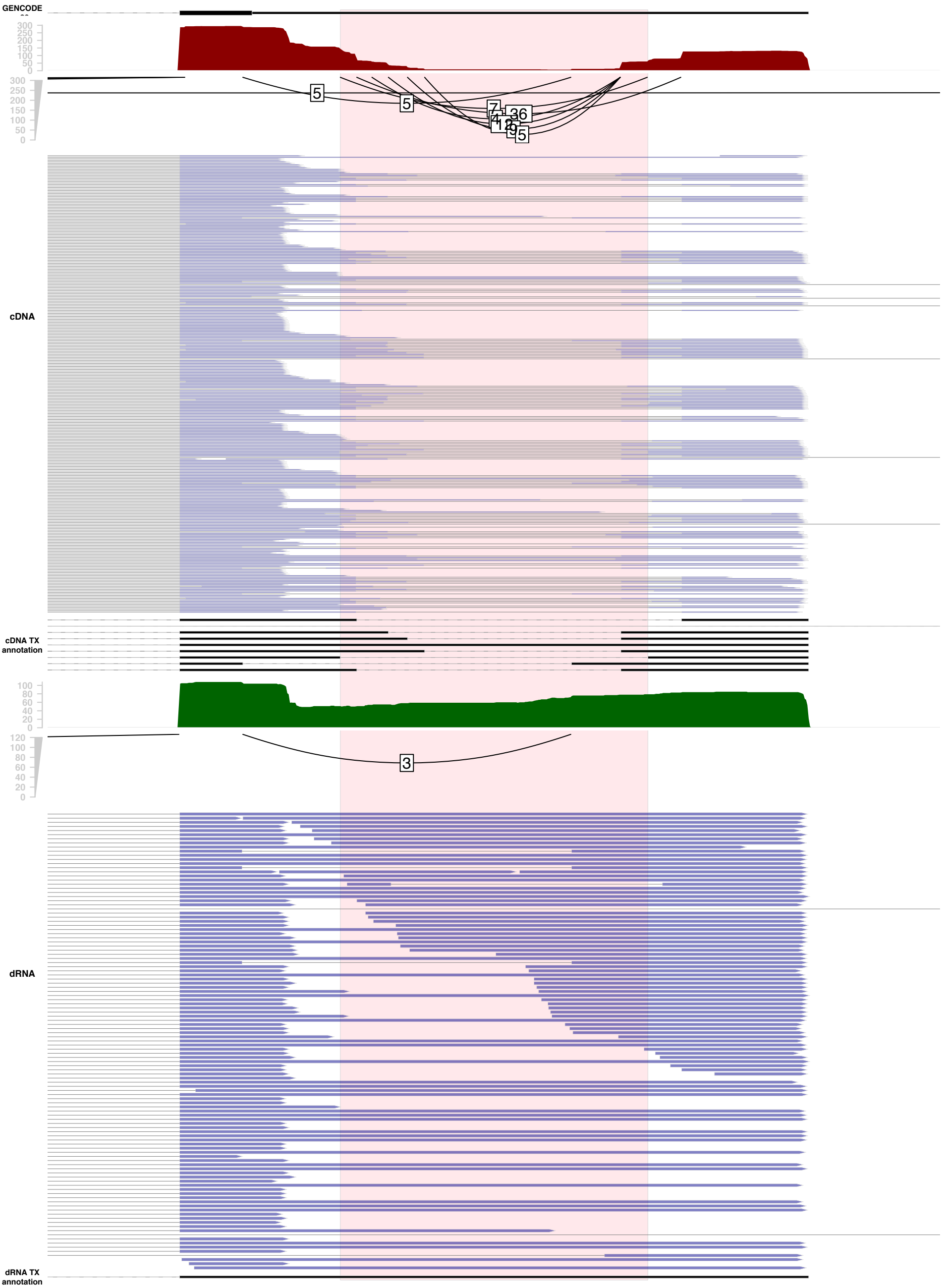
Cell line: NA12878



chr6:70588859-70589325:+ SDHAF4

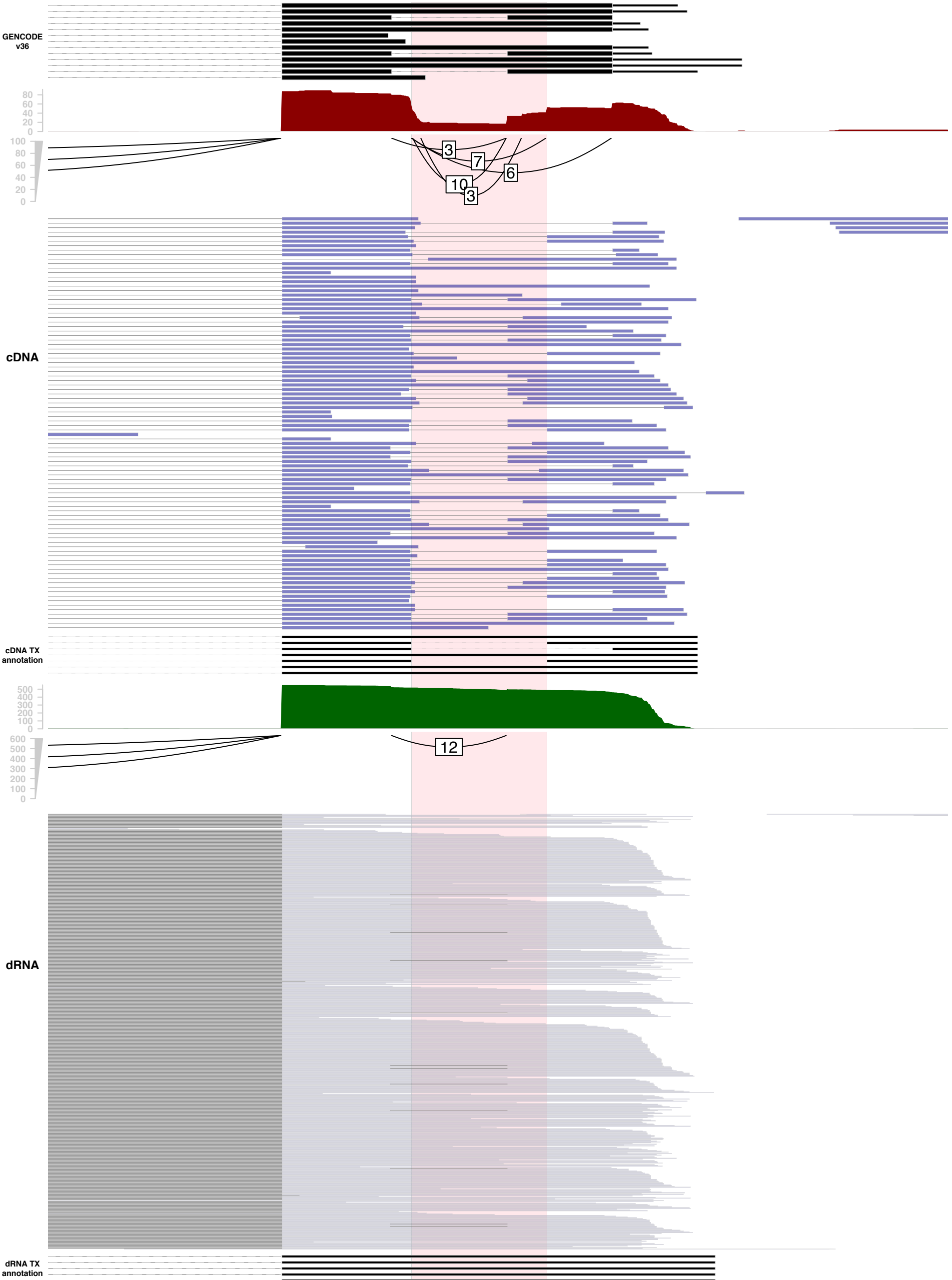
Cell line: NA12878

Direct repeat sequence: TGGCT



chr6:170584410-170584525:- PDCD2

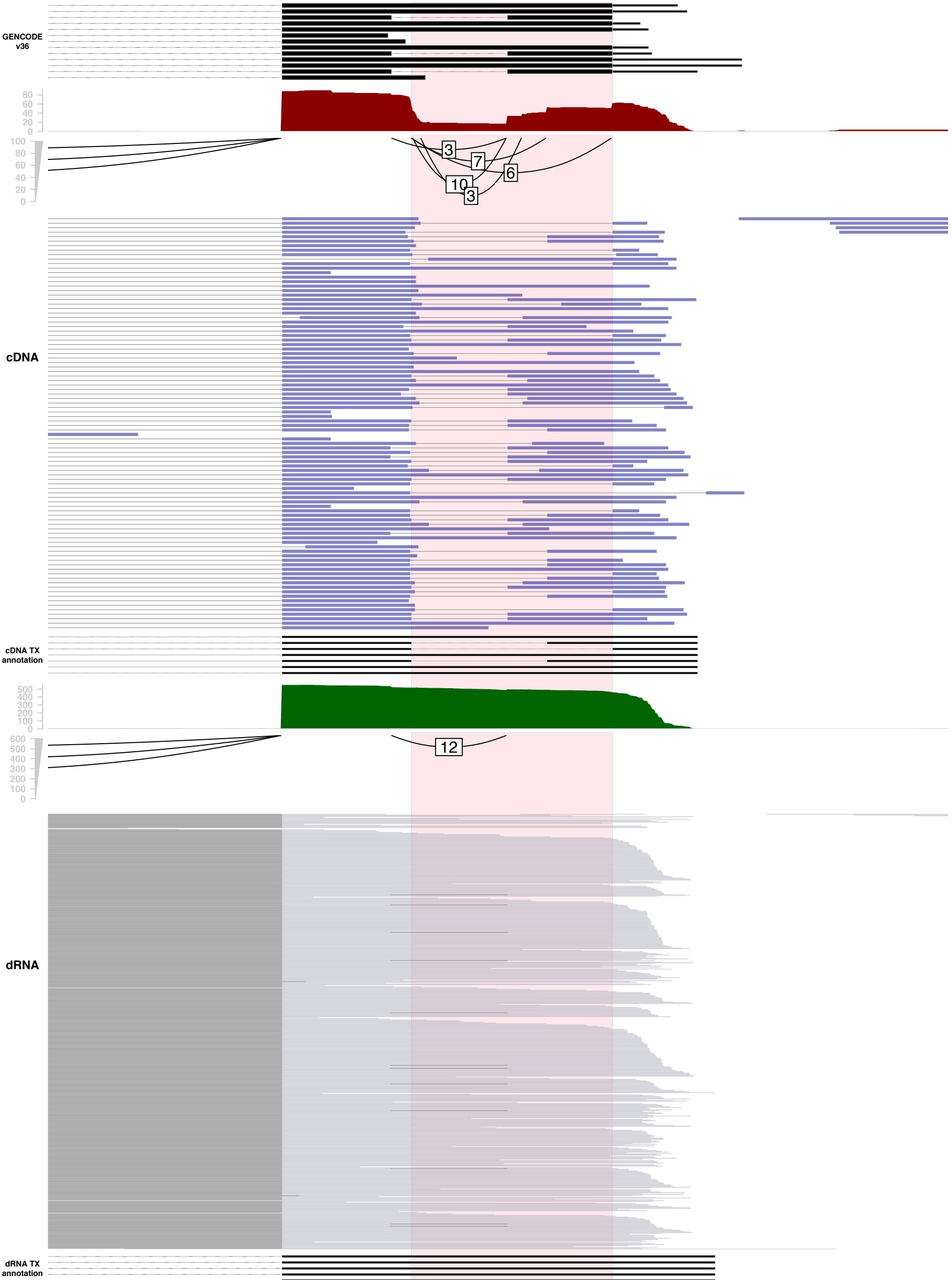
Cell line: NA12878



chr6:170584410-170584581:- PDCD2

Cell line: NA12878

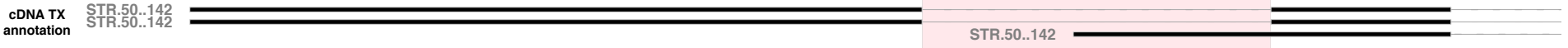
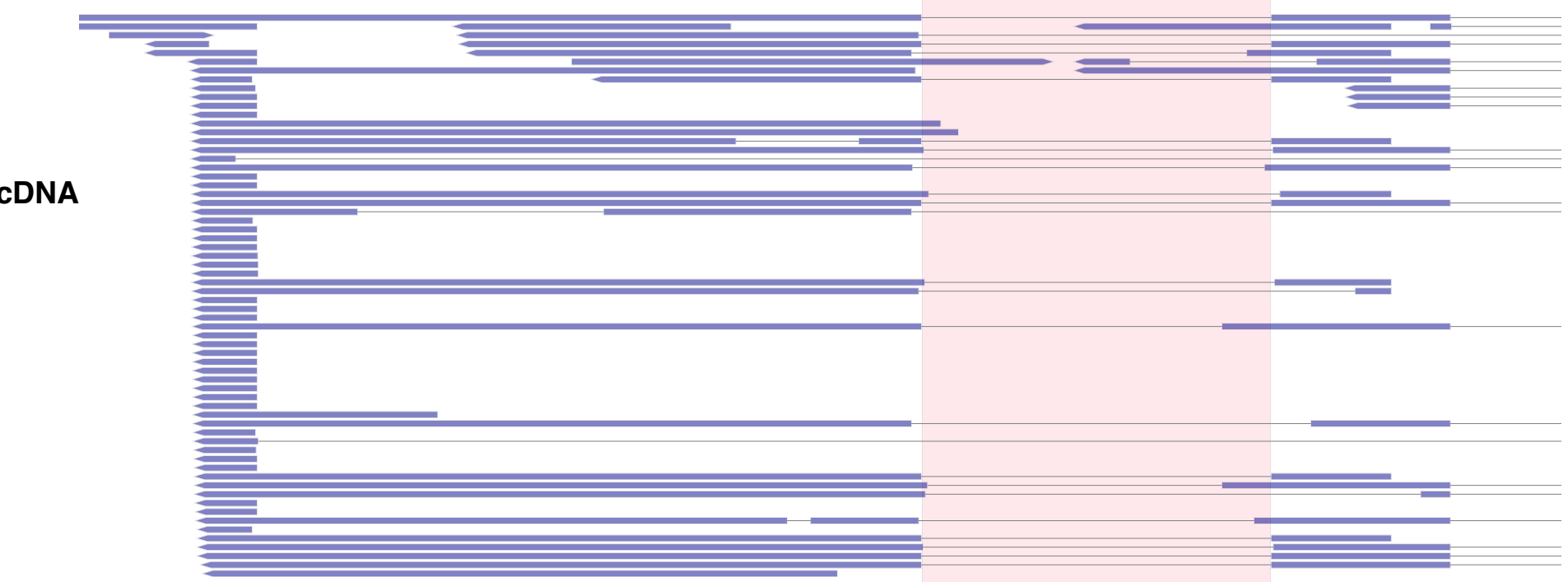
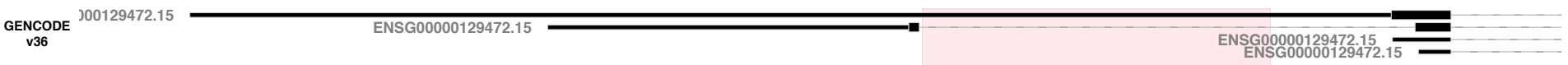
Direct repeat sequence: CCCGC



chr14:21460346-21460977:- RAB2B

Cell line: NA12878

Direct repeat sequence: CCTCC

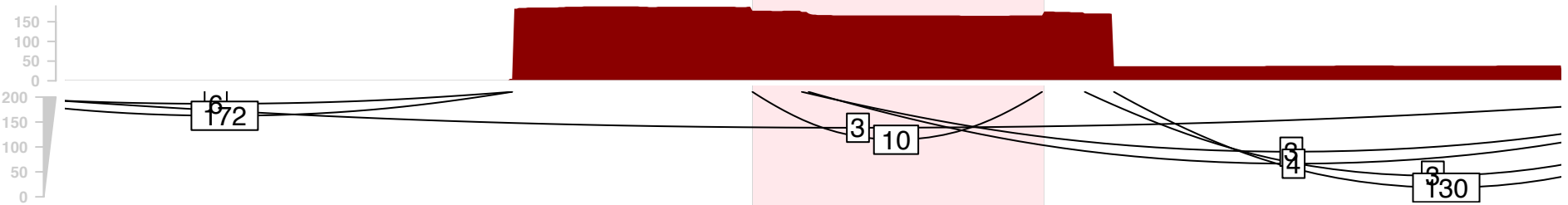


chr16:28932452-28932581:+ CD19

Cell line: NA12878

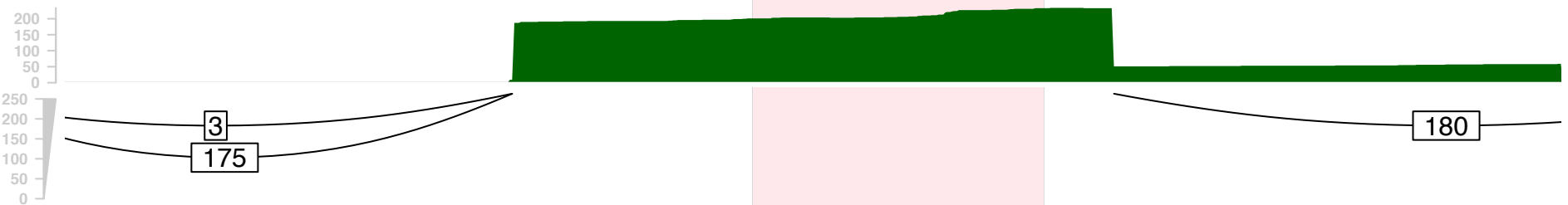
Direct repeat sequence: CAGCCTGG

GENCODE v36



cDNA

cDNA TX annotation



dRNA

dRNA TX annotation

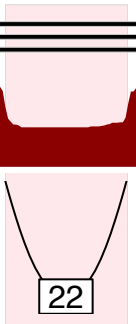


chr17:3663563-3663657:- TAX1BP3,P2RX5-TAX1BP3

Cell line: NA12878

Direct repeat sequence: GACCG

GENCODE v36
ENSG00000213977.8
ENSG00000213977.8
ENSG00000257950.3



68

cDNA



cDNA TX annotation

STR:58..450



96

dRNA



dRNA TX annotation

STR:90..80